/home/fuller/feb1098/US-08-836-075A-2 rag

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kh J, Miller RH, Purcell RH;
1; 96-139709/14.
SSDB; T16650.
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\ and amino acid sequence of HCV envelope I and core proteins -id to determine HCV genotype and as vaccines against HCV infection inm 4; Page 214; 340pp; English.
//36-R92987 are HCV core proteins derived from 52 different HCV lates Isolated coMA sequences are used for the produ of primers ful for detecting the presence of HCV in a sample, the primers also useful for HCV genotyping. Proteins encoded by the CDNAs be used in vaccines for immunising against HCV infection. The teins may also be used to detect antibodies against HCV in serum, iva, lymphocytes or other mononuclear cells. The antibodies may pased in the prevention of HCV infection.

ö 9; Indels 0; Gaps Length 191; Score 777; DB 17; Pred. No. 2.12e-61; 1; Mismatches Match 99.5%; ocal Similarity 90.8%; 99; Conservative

mstnpkpqrktkrntnrrpmdvkfpgggivggvyllprrgprlgvratrktsersqprg 60

l rrqpipkarrsegrswaqpgypwplygnegcgwagwllsprgsrpswgp 109

ntitis C virus isolate 28 core protein.

El; envelope 1; core protein; HCV genotyping; antibody; vaccine; 4 373 standard; Protein; 191 AA. CT-1996 (first entry) titis C virus.

TEB-1996. .UC-1995, U10398. .UC-1994, US-290665. Н) US DEPT HEALTH & HUMAN SERVICES. Н) US SEC DEPT HEALTH.

J, Miller RH, Purcell RH; 96-139709/14.

DB: 716647.

and amino acid sequence of RCV envelope 1 and core proteins - to determine HCV genotype and as vaccines against HCV infection m 4; Page 211-212; 340pp; English.

35-R92987 are HCV core proteins derived from 52 different HCV

ates. Isolated cDNA sequences are used for the prodn. of primers ul for detecting the presence of HCV in a sample, the primers iso useful for HCV genotyping. Proteins encoded by the CDNNs are used in vaccines for immunising against HCV infection. The man may also be used to detect antibodies against HCV in serum, 12, lymphocytes or other monounclear cells. The antibodies may red in the prevention of HCV infection.

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61 rrqpipkarrsegrswaqpqypwplygnegcgwagwllsprgsrpswgp 109 셤 ð

61 RROPIDEGERSKAGPCYPMPLYQNEGGGRAXWLLSPRGSRPNWGP 109

A hepatitis C virus gene and oligo-nucleotide(s) - used for the Hepatitis C virus SR037-5' gene product. Hepatitis C virus; HCV; non-A non-B; SR037-5'; treatment. Hepatitis C virus. ur 5 R67591 standard; Protein; 502 AA. 07-SEP-1995 (first entry) 13-MAY-1993; 147133. 13-MAY-1993; JP-147133. (IMMO) IMMUNO JAPAN KK. WP1; 95-040318/06. N-PSDB; Q79143. 22-NOV-1994. J06319563-A. R67591;

treatment of hepatitis C Claim 21; Page 36; 41pp; Japanese. 079143 is the hepatitis C virus (HCV) gene SR037-5' CDNA, it encodes the protein described in R67591. Both the CDNA and protein can be used in the treatment of HCV infection Sequence 502 AA;

9; Indels 0; Gaps Query Match 99.5%; Score 777; DB 12; Length 502; Best Local Similarity 90.8%; Pred. No. 2.12e-61; Matches 99; Conservative 1; Mismatches 9; Indels 1; Mismatches

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61 rrqpipkarrpegrewaqpgypwplygnegcgwagwlleprgsrpswgp 109 61 RROPIPKAXRXEGRSWAQPGYPWPLYGNEGCGMAXWLLSPRGSRPWNGP 109 윱 ð

Hepatitis C virus YS117-5' gene product. Hepatitis C virus; HCV; non-A non-B; YS117-5'; treatment. R67589 standard; Protein; 502 AA. 07-SEP-1995 (first entry) 13-HAY-1993; 147133, 13-HAY-1993; JP-147133, (IMHO) IMHUNO JAPAN KK, WPI; 95-040318/06, Hepatitis C virus. J06319563-A 22-NOV-1994 R67589; RESULT AC DE PROPERTO DE

A hepatitis C virus gene and oligo-nucleotide(s) - used for the treatment of hepatitis C N-PSDB; Q79141.

Claim 19; Page/34; 41pp; Japanese. Q79141 is the hepatitis C virus (HCV) gene YS117-3' CDNA, it encod the protein described in R67588. Both the cDNA and protein can be used in the treatment of HCV infection

502 AA; Sequence Mome/fuller/feb1098/US-08-836-075A-1.rge

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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
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                                                                                                                                                               Maertens G., Stuyver L.;
"NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE
                                                                                                                                                                                       AS PROPHYLACTIC, THERABEDTIC AND DIAGNOSTIC AGENTS';
Patent number W09613590-A/1, 09-MAY-1996.
INNOGENETICS NV (BE).
Other publication AU 3844095 960523
                                                                                                                                                                                                                                                                                       /organism="unidentified"
Sequence 327 BP; 56 A; 102 C; 104 G; 51 T; 14 other;
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Hepatitis C virus core gene, HN3 isolate.
                                                     07-MAR-1997 (Rel. 51, Created)
07-MAR-1997 (Rel. 51, Last updated, Version 1)
Sequence 1 from Patent W09613590.
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Qu.D., FRANCE
2 (bases 1 to 506)

Qu.D., Hantz,O., Gouy,M., Vitvitski,L., Li,J.S., Berby,F., Herronoviter of the control of the c
                                                                                                  Submitted (22-NOV-1993) to the EMBL/GenBank/DDBJ databases. D. Qu, INSERW Unite 271, U. de Recherche sur les Hepatites,, le Sida et
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Hepatitis_G-like viruses.
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J. Gen. Virol. 75 (Pt 5), 1063-1070 (1994)
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standard; DNA; UNC; 327

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                                         Submitted (22-NOV-1993) to the EMBL/GenBank/DDBJ databases. D. Qu, INSERM Unite 271, U. de Recherche sur les Hepatites,, le Sida et les Retrovirus Humains, 151 cours Albert Thomas, F 69424 Lyon Cedex
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Qu.D., Hantz, O., Gouy, M., Vitvitski, L., Li, J.S., Berby, F., Tong, S.P. and Trepo, C.
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Score 317; DB 143; Length 327; Pred. No. 7.68e-244;

Query Match 100.0%; Best Local Similarity 100.0%; Matches 327; Conservative

Sequence 327 BP; 56 A; 102 C; 104 G; 51 T; 14 other;

/organism="unidentified"

source

0; Mismatches 0; Indels

NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE

Maertens G., Stuyver L.;

unclassified unidentified

07-MAR-1997 (Rel. 51, Created) 07-MAR-1997 (Rel. 51, Last updated, Version 1) Sequence 1 from Patent W09613590.

AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS"; Patent number W09613590-A/1, 09-MAY-1996. INNOGENETICS NV (BE).

Other publication AU 3844095 960523

Location/Qualifiers

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ggccccaggnngggtgtgcgcgcgactaggaagacttccgagcggtcacaacctcgtggc 180

aggogacagoctatococaaggotogycggycogagggoaggtootgggotoagcooggg 240 AGCCACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCCAGGTCCTGGGCTCAGCCCGGG 240

181 181 241 241 301 301 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Hepatitis C-like viruses.

OCUS HCVHN3 506 bp DNA VERINITION Repátitis C virus core gene, HN3 isolate.

core; core protein. Hepatitis C virus.

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Hepatitis C virus

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Feb 23 11:05:49 1998; Maskar time 2.74 Seconds 202.390 Million cell updates/sec Run on:

Title:

Tabular output not generated.

Description: Perfect Score:

>US-08-836-075A-2 (1-109) from US08836075A.pep 781 1 MSTNPKPQRKTKRNTNRRPX..........GCGMAXWLLSPRGSRPNWGP 109 Sequence:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Mean 26.601; Variance 124.684; scale 0.213 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		o,							
	Score	Query Match	Query Match Length DB	93	ΟI	Description	Ë	_	Pred. No.
i	רוו	99.5	191	13	PCT-US95-1	Sequence 1	195, A	Applicat	2.00e-59
	777	99.5	191	13	PCT-US95-1	Sequence 1	192, A	Applicat	2.00e-59
	175	99.5	191	13	PCT-US95-1			Applicat	3.03e - 59
	775	99.5	191	13	PCT-US95-1	Sequence 1	_	Applicat	3.03e-59
	775	99.5	191	13	PCT-US95-1	Sequence 1	_	Applicat	3.03e - 59
	775	99.5	191	13	PCT-US95-1	Sequence 1	196, A	Applicat	3.03e-59
	775	99.5	191	13	PCT-US95-1	Sequence 1		Applicat	3.03e - 59
	775	99.5	191	Ξ	PCT-US95-1	Sequence 1		Applicat	3.03e - 59
	775	99.5	196	12	PCT-US94-0	Sequence 1	13, Ap	pplicati	3.03e-59
	175	99.5	196	13	PCT-US95-0	Sequence	13, Ap	Applicati	3.03e-59
	775	99.5	196	7	US-08-188-	Sequence 1	13, Ap	pplicati	3.03e-59
	. 775	99.5	1648	13	PCT-US95-0	Sequence	12, Ap	pplicati	3.03e - 59
	775	99.2	1648	12	PCT-US94-0	Sequence	12, Ap	pplicati	3.03e-59

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ce 12, Applicati	٦,	-;	ce 1, Applicatio	2,	۳,	۲,		193	155,	197,	19	7, A	36	10,	36,	18,	18,	16,	16,	194,	14, }	12,	12,	14,	10, A	176,		166,	12,		ce 4, Applicatio
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-188-	PCT-US94-0	PCT-US95-0	PCT-US93-0	PCT-US93-0	US-08-453-	US-08-453-	US-08-188-	PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US92-0	US-08-440-	US-07-910-	US-08-440-	US-07-681-	PCT-US91-0	PCT-US91-0	US-07-681-	PCT-US95-1	US-07-681-	PCT-US91-0	US-07-681-	PCT-US91-0	PCT-US91-0	PCT-US95-1	PCT-US95-1	PCT-US95-1	US-07-910-	US-07-681-	US-08-143-
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99.5	99.5	99.5	99.5	99.2	99.5	99.5	3.66	99.1	98.6	98.5	98.5	98.0	98.0	0.86	0.86	97.6	97.6	97.6	97.6	97.6	97.6	9.76	91.6	97.6	97.4	8.96	96.5	96.5	96.5	96.4	96.4
775	775	775	775	775	775	775	775	174	770	169	169	765	765	765	765	762	162	762	162	162	762	762	762	762	761	756	754	754	754	753	753
14	15	16	17	18	19	70	21	22	23	. 24	52	56	27	58	58	30	31	32	33	34	35	36	31	38	39	40	41	42	43	44	45

ALI GNMENTS

home/fuller/feb1098/LIS-08-836-075A-2.rai

Feb 23 11:03

ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

CORRESPONDENCE ADDRESS:

APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995

SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/086,428 FILING DATE: 29 JUNE 1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/290/665

PRIOR APPLICATION DATA:

CLASSIFICATION:

FILING DATE: 15 AUGUST 1994 ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK

1 MSTNPKPORKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60 Indels 0; Gaps Query Match 99.5%; Score 777; DB 13; Length 191; Best Local Similarity 90.8%; Pred. No. 2.00e-59; 61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109 61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109 191 AA 6 1; Mismatches REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849 PRT; Sequence 158, Application PC/TUS9510398. ORGANISM: homosapiens INDIVIDUAL ISOLATE: 28 ICE 191 AA; 20744 MW; 181593 CN; REGISTRATION NUMBER: 36,459 INFORMATION FOR SEQ ID NO: 192: STANDARD; LENGTH: 191 amino acids SEQUENCE CHARACTERISTICS: STRANDEDNESS: unknown 99, Conservative TOPOLOGY: unknown amino acid TELEX: 421792 ORIGINAL SOURCE: PCT-US35-10398-158 01-JAN-1900 XXXXXX Matches RESULT ð a à 2 X E X E X S

61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109

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191 AA

STANDARD;

PCT-US95-10398-192

RESULT

01-JAN-1900

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1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

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Sequence 158, Application PC/TUS9510398

AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF 1SO!ATSS OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF INVENTION: NO TITLE OF INVENTION: AS TITLE OF INVENTION: AS TITLE OF INVENTION: AS TITLE OF INVENTION: SI NUMBER OF SEQUENCES:

NUCLEOTIDE AND DEDUCED

APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.

Sequence 192, Application PC/TUS9510398 GENERAL INFORMATION: Sequence 192, Application PC/TUS9510398.

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home/fuller/feb1098/US-08-836-075A-2.rai

191 AA

PRT;

STANDARD;

PCT-US95-10398-156

ö APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIBUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES 0; Gaps Length 191; Indels Query Match 99.2%; Score 775; DB 13; Best Local Similarity 89.9%; Pred. No. 3.03e-59; 2; Mismatches REFERENCE/DOCKET NUMBER: 2026-4116 APPLICATION NUMBER: PCT/US95/10398 Sequence 156, Application PC/TUS9510398 FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION: Sequence 156, Application PC/TUS9510398. ORGANISM: homosapiens INDIVIDUAL ISOLATE: US11 ICE 191 AA; 20766 WW; 182089 CN; MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428 ADDRESSEE: MORGAN & FINNEGAN RECISTRATION NUMBER: 36,459 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800 FILING DATE: 15-AUG-1995 (212) 751-6849 LENGTH: 191 amino acids 345 PARK AVENUE CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: RICHARD W. BORK CORRESPONDENCE ADDRESS: STRANDEDNESS: single TOPOLOGY: unknown COMPUTER READABLE FORM: 98; Conservative NUMBER OF SEQUENCES: TYPE: amino acid GENERAL INFORMATION: STATE: NEW YORK CLASSIFICATION: CITY: NEW YORK TELEX: 421792 COUNTRY: USA ORIGINAL SOURCE 10154 TELEFAX: STREET: NAME: 01-JAN-1900 SEQUENCE XXXXXX Matches

Feb 23 11:03

TELEPHONE: (212) 758-4800 01-JAN-1900 SEQUENCE XXXXXX Matches RESULT 8 8 8 ð ð NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109 Z APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. 2026-4116 APPLICATION NUMBER: PCT/US95/10398 Sequence 157, Application PC/TUS9510398 Sequence 157, Application PC/TUS9510398 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: 08/290/665 FILING DATE: 15 AUGUST 1994 ATTORNEY/AGENT INFORMATION: NAME: RICHARD W. BORK PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/086,428 ADDRESSEE: MORGAN & FINNEGAN REGISTRATION NUMBER: 36,459 REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 157: FILING DATE: 29 JUNE 1993 PRIOR APPLICATION DATA: SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: STANDARD; TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 FILING DATE: 15-AUG-1995 LENGTH: 191 amino acids STREET: 345 PARK AVENUE SEQUENCE CHARACTERISTICS: STRANDEDNESS: unknown CORRESPONDENCE ADDRESS: TITLE OF INVENTION: PTITLE OF NUMBER OF SEQUENCES: TOPOLOGY: unknown ORIGINAL SOURCE: TYPE: amino acid STATE: NEW YORK GENERAL INFORMATION: CLASSIFICATION: CITY: NEW YORK TELEX: 421792 COUNTRY: USA PCT-US95-10398-157 ZIP: 10154 01-JAN-1900 XXXXX RESULT දු 3

ö 1 MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60 Indels 0; Gaps Score 775; DB 13; Length 191; Pred. No. 3.03e-59; 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109 61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109 2; Mismatches 191 AA; 20766 MW; 182089 CN; ORGANISM: homosapiens Query Match 99.2%; Best Local Similarity 89.9%; 98; Conservative

191 AA NUCLEOTIDE AND DEDUCED APPLICANT: BUKH, J., MILLER, R.H. AND PRT; Sequence 196, Application PC/TUS9510398 Sequence 196, Application PC/TUS9510398. STANDARD; APPLICANT: PURCELL, R.H. TITLE OF INVENTION: GENERAL INFORMATION: PCT-US95-10398-196

AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES REGISTRATION NUMBER: 36,459 REFERENCE/DOCKET NUMBER: 2026-4116 TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398 MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/290/665 APPLICATION NUMBER: 08/086,428 ADDRESSEE: MORGAN & FINNEGAN FILING DATE: 15 AUGUST 1994 ATTORNEY/AGENT INFORMATION: FILING DATE: 29 JUNE 1993 TITLE OF INVENTION: CORE GITTLE OF INVENTION: CORE GITTLE OF INVENTION: SEQUENTIALE OF INVENTION: SEQUENCES: 263
CORRESPONDENCE ADDRESS: FILING DATE: 15-AUG-1995 345 PARK AVENUE NAME: RICHARD W. BORK PRIOR APPLICATION DATA: COMPUTER READABLE FORM: STATE: NEW YORK CLASSIFICATION: CITY: NEW YORK COUNTRY: USA ZIP: 10154

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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNASTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                     1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRTTRKTSERSQPRG 60
                                                                                                                                                                                                            0;
                                                                                                                                                                              Score 775; DB 13; Length 191;
Pred. No. 3.03e-59;
                                                                                                                                                                                                                                                                                                            61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109
                                                                                                                                                                                                                                                                                              61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                191 AA
                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/10398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 159, Application PC/TUS9510398.
                                                                                                                                                     191 AA; 20788 MW; 180939 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/086,428
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             TELEX: 421792
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-AUG-1995
(212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 263
                                                                                                                                       INDIVIDUAL ISOLATE: 27
                                                                                 STRANDEDNESS: unknown
                                                                                                                            ORGANISM: homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                               Query Match 99.2%;
Best Local Similarity 89.9%;
                                                                                                                                                                                                             98; Conservative
                                                                                                TOPOLOGY: unknown
                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
                                                                                                              ORIGINAL SOURCE:
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE EQUENCES OF THE ENVELOPE I AND
TITLE OF INVENTION: CORE CENES OF ISOLATES OF HEPATITIS C VINUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                     1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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home/fuller/feb1098/US-08-836-075A-2.rai
                                                                                                                                                                                                                                                                                                                                            Query Match 99.2%; Score 775; DB 13; Length 191;
Best Local Similarity 89.9%; Pred. No. 3.03e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RRQPIPKAXRXECRS#AQPGYP#PLYGNEGCG#AX#LLSPRGSRPW#GP 109
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                     2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160, Application PC/TUS9510398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 160, Application PC/TUS9510398.
                                                                                                                                                                                                                                                                                        ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S18
ICE 191 AA; 20766 MM; 182089 CN;
                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/290/665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                           FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                      REGISTRATION NUMBER: 36,459
                                                                                                                                                                        TELEX: 421792
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 263
                                                                                                                                                                                                                                              STRANDEDNESS: unknown
                                                                                         NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK
                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-10398-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1900
                                                                                                                                                                                                                                                                                                                      SEQUENCE
   Feb 23 11 03
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SEOUENCE Query Match

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Mome#uller/feb1098/US-08-836-075A-2.rai
                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US94/07280
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                        ONE ABBOTT PARK ROAD
     Feb 23 11:03
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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60 Gaps ö Query Match 99.2%; Score 775; DB 12; Length 967; Best Local Similarity 89.9%; Pred. No. 3.03e-59; 61 RRQPIPKARRPEGRIWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109 61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109 9; Indels 2; Mismatches

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967 AA PRT; Sequence 13, Application PC/TUS9501087 GENERAL INFORMATION: Sequence 13, Application PC/TUS9501087.

PCT-US94-07280-13

RESULT

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APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGCVYLLPRRGPRLGVRATRKTSERSQPRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 775; DB 7; Length 967;
Pred. No. 3.03e-59;
                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: POREMBSKI, PRISCILIA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HENCE 967 AA; 106397 MW; 5014170 CN;
                                                                                                                                                                       APPLICATION NUMBER: US/08/188, 281B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application PC/TUS9501087 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application PC/TUS9501087.
                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WATANABE, SHINICHI APPLICANT: YAMAGUCHI, JULIE
                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DESAI, SURESH M. APPLICANT: DEVARE, SUSHIL G.
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 967 amino acids
                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                       single
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Best Local Similarity 89.9%;
                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ABBOTT PARK
ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sin
TOPOLOGY: linear
                                  RY: USA
60064-3500
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-01087-12
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV IIILE OF INVENTION: ENVELOPE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 775; DB 13; Length 967;
Pred. No. 3.03e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWMGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             967 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEPHONE: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HENCE 967 AA; 106397 MW; 5014170 CN;
                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/01087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08188281B
Patent No. 5610009
GEMERAL INFORMATION:
APPLICANT: WATANABE, SHINICHI
APPLICANT: YAMAGUCHI, JULLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08188281B.
                                                                                                                                                                                                                                              NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEVARE, SUSHIL G.
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         single
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Best Local Similarity 89.9%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                   COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-188-281B-13
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Query Match

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APPLICANT: WATANABE, SHINICHI
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVAILS SURESH M.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08188281B
Patent No. 5610009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08188281B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WAPANDE, SHINICHI
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: DESAI, SUBESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: BAWALLIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   Query Match 99.2%; Score 775; DB 13; Length 1648; Best Local Similarity 89.9%; Pred. No. 3.03e-59; Matches 98; Conservative 2; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                              NAME: POREMBSKI, PRISCILLA E.
RECISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
TELECOMMUNICATION INFORMATION:
TELECHONE: 708-931-6565
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FENCE 1648 AA; 178869 MW; 14581021 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                  APPLICATION NUMBER: PCT/US95/01087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS9407280 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application PC/TUS9407280
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
          COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          LENGTH: 1648 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                          CLASSIFICATION:
                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ST 13
PCT-US94-07280-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                              COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1648 AA.
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Pred. No. 3.03e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE 1648 AA; 178869 MW; 14581021 CN;
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILIA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
                                                                                                                                                        APPLICATION NUMBER: PCT/US94/07280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1648 amino acids
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                                                                                                                                                                                                                                                                                                                                TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 99.2%;
Local Similarity 89.9%;
nes 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-188-281B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

60064-3500

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188, 281B

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07280

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01

TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365 TELEFAX: 708-938-2623

REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEPAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:

LENGTH: 1648 amino acids

STRANDEDNESS: single

TOPOLOGY: linear amino acid

ATTORNEY/AGENT INFORMATION: NAME: POREMBSKI, PRISCILLA E.

8555555555555555555555555555555

CLASSIFICATION: 435

FILING DATE:

INFORMATION FOR SEQ ID NO: 1:

LENGTH: 3011 amino acids SEQUENCE CHARACTERISTICS: TYPE: amino acid

STRANDEDNESS: single TOPOLOGY: linear

MOLECULE TYPE: protein JENCE 3011 AA; 327108 MW; 47577590 CN; SEQUENCE

Gaps ; 0 Query Match 99.2%; Score 775; DB 12; Length 3011; Best Local Similarity 89.9%; Pred. No. 3.03e-59; Matches 98; Conservative 2; Mismatches 9; Indels 0;

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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60 a ð

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Gaps

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Score 775; DB 7; Length 1648; Pred. No. 3.03e-59;

Query Match 99.2%; Best Local Similarity 89.9%; Matches 98; Conservative

MOLECULE TYPE: protein SEQUENCE 1648 AA; 178869 MW; 14581021 CN;

2; Mismatches 9; Indels

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3011 AA.

PRT;

STANDARD;

PCT-US94-07280-1

RESULT ≘≍ 01-JAN-1900

XXXXXX

61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109 g

61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGGGWAXWLLSPRGSRPNWGP 109 à

Search completed: Mon Feb 23 11:06:01 1998

Job time : 12 secs.

APPLICANT: WATANABE, SHINICHI
APPLICANT: WATANABE, SHINICHI
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES
NUMBER OF SOGUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD

ABBOTT PARK

COUNTRY: USA

STATE: IL

Sequence 1, Application PC/TUS9407280 GENERAL INFORMATION: Sequence 1, Application PC/TUS9407280.

. Feb 23.1102

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Feb 23 11:03:09 1998; MasPar time 11.95 Seconds 226.191 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-836-075A-2 (1-109) from US08836075A.pep 781 Description: Perfect Score:

1 MSTNPKPQRKTKRNTNRRPX......GCGWAXWLLSPRGSRPNWGP 109 Sequence:

PAM 150 Scoring table:

243240 seqs, 24799054 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-pending
1:PCT91 2:PCT92 3:PCT93 4:PCT94 5:PCT95 6:PCT96 7:PCT97
8:U73 9:U76 10:U77A 11:U77B 13:U78B 14:U79B
15:U79B 16:U800 17:U801 18:U802 19:U803 20:U804 21:U805
22:U806 23:U807 24:U808 25:U819 26:U810 27:U811 28:U812
29:U813 30:U814 31:U815 32:U816 33:U817 34:U818 35:U819
36:U820 37:U821 38:U822 39:U823 40:U824 41:U825 42:U826
43:U827 44:U828 45:U829 46:U830 47:U821 48:U832 49:U833
50:U843 51:U835 52:U836 53:U837 54:U838 55:U840
57:U841 58:U842 59:U843 60:U844 61:U845 62:U846
71:U60 72:URMP 73:URMU6 74:URMU8

Mean 27.872; Variance 128.076; scale 0.218

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.66e-60 1.32e-59 1.32e-59 1.32e-59
bescription	Sequence 2, Applicatio Sequence 28, Applicati Sequence 195, Applicat Sequence 192, Applicat
Descri	
ID	US-08-836- US-08-836- US-08-290- US-08-290-
80	74 74 45
* Query Match Length DB	109 74 117 74 191 45 191 45
% Query Match	100.0 99.5 99.5 99.5
* esult Query No. Score Match L	181 777 777
Result No.	4 3 2 1

2.0	2.0le-	2.0le-	2.01e-	2.01e-	2.01e-	2.01e-	2.01e-	2.01e-	2.01e-	, 2.01e-	2.01e-	2.01e-	2.01e-	o 2.01e-	2.01e-	2.48e-	4.67e-	5.77e-	5.77e-	5.77e-	.77e-	7.13e-	7.13e-	1.66e-	1.66e-	, 1.66e-	1.66e-	1,66e-	1.666	1.66e-	1.66e-	. 1.66e-	1.66e-	1.66e-	1.66e-	2.05e-	cati 2.53e-	icati 2.53e-
Sequence 6, Appl	15	9.	Sequence 3, Appl.	equence 16	equence 15	equence 15	23	-,	2,	_;	2,	20	-;	equence 2,	7	13	12	19	Ļ,	-;	13	Sequence 191, App	19	9	7,	'n	7	~	equence 2,	equence 36	Sequence 36, App.	496	36,	10,	10,	~	30,	11,
07	80	200	-08-380	-08-2	80-	-08-	-08-2	-08-7	-08-	-08-4	4	8-80-	-08-4	-08-4	8-80-	-08-	8-80-	-08-3	-08-	0-80-	-08-	8-2	-08	-08-3	98-4	r-us9	-07-9	8	-08	-08-4	-08-2	07-7	-08-4	-08 - 44	-08-4	-08-7	-07-79	-07-8
120 11															3012 69	191 45	319 74	166 52	190 23	190 23	191 45	191 45	191 45	166 52	396 62	396 2	396 15	396 62	396 69	3011 63	3011 39	3011 10	3011 60	3011 60	3011 60	218 68	513 11	733 13
2.66	99.2	2.66	2.66	99.2	99.2	99.2	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.1	98.7	98.6	98.6	98.6	98.6	98.5	98.5	98.0	0.86	0.86	0.86	98.0	98.0	0.86	98.0	0.86	0.86	0.86	0.86	97.8	7.76	97.7
775	51.	57.7	277	775	775	775	775	775	775	115	115	775	775	775	775	174	111	170	770	170	770	169	169	755	765	765	765	765	765	765	765	765	765	765	765	764	763	763
20 4	، م	- 0	စေ	10	11	12	13	14	15	16	11	18	19	20	71	22	73	24	52	56	27	88	59	9	31	32	33	34	32	36	37	38	39	40	41	42	43	44

	109 AA.												TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES	AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DI
Ē	PKI						5A.		15A				NCES 0	USE A
	STANDARD;						12/0883607		US/088360		GEERT	LIEVEN	NEW SEQUE	AND THEIR
							oplication U		Application	NWATION:	APPLICANT: MAERTENS, GEERT	APPLICANT: STUYVER, LIEVEN	INVENTION:	TITLE OF INVENTION:
1	US-U8-836-U / DV-7		xxxxx		01-JAN-1900		Sequence 2, Application US/08836075A.		Sequence 2, Application US/08836075A	GENERAL INFORMATION:	APPLICANT:	APPLICANT:	TITLE OF 1	TITLE OF 1
RESULT 1	10 05	×	AC xx	XX	DT 01	×	DE Se	×	S S	ಟ	బ్ర	ಟ	ප	ខ

ALIGNMENTS

TITLE OF INVENTION: AGENTS NUMBER OF SEQUENCES: 207 CORRESPONDENCE ADDRESS: AGNOSTIC ខ្លួន

Feb 23:11:02

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TITLE OF INVENTION: AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSTNPKPQRKTKRNTNRRPXXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 781; DB 74; Length 109;
Pred. No. 5.66e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQP IPKAXRXEGRSWAQP CYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                  SOFTWARE: Microsoft Word 6.0 / ASCII text output
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
                                                                                                                                                             APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 95870076.7 FILING DATE: 28 Jun 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 2:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/08836075A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
JENCE 109 AA; 12273 MW; 64913 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08836075A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MAERTENS, GEERT APPLICANT: STUYVER, LIEVEN TITLE OF INVENTION: NEW SEC TITLE OF INVENTION: AND THE
                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                 CURRENT APPLICATION DATA:
            P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                               77210-4433
                           HOUSTON
                                         TEXAS
                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-836-075A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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Pred. No. 1.32e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word 6.0 / ASCII text output CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BUKH, J., MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/EP95/04155
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 94870166.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 195, Application US/08290665A
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 195, Application US/08290665A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
SEQUENCE 117 AA; 13380 MW; 67911 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21 Oct 1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23 Oct 1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 117 amino acids
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Mat:h
Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100; Conservative
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                     ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                     HOUSTON
                                                                                                            STATE: TEXAS
                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-290-665A-195
                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1900
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Feb 23.11:02

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NUCLEOTIDE AND DEPYCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE CENES OF 1SOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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Pred. No. 1.32e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RROPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/290, 665A FILING DATE: 15-AUG-1994
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homosapiens
INDIVIDUAL ISOLATE: 26
ICE 191 AA; 20774 MM; 184617 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 192, Application US/08290665A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 192, Application US/08290665A
                                                                                               ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 421792
INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 191 amino acids
                                                                    NUMBER OF SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.5%;
Best Local Similarity 90.8%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                        STATE: NEW YORK
                                                                                                                           CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-290-665A-192
                                                                                                                                                                   ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1900
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home/fuller/feb1098/13S-08-836-075A-2.rap Feb 23 11:02

MILLER, R.H. AND

GENERAL INFORMATION:

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                                                     CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                           AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                    R.H.
NUCLEOTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 777; DB 45;
Pred. No. 1.32e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homosapiens
INDIVIDUAL ISOLATE: 28
ICE 191 AA; 20744 MW; 181593 CN;
                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                     TELEFHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                         263
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: unknown
                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Conservative
        APPLICANT: BUKH, J., APPLICANT: PURCELL, I
                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                 STATE: NEW YORK
                                                                                                                                      NEW YORK
                                                                                                                                                                                                                                                                                                                                                                             TELEX: 421792
                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                        ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-786-169A-6
                                                                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
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Feb 23.11:02

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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF HEE REVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 775; DB 45;
Pred. No. 2.01e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                  APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2026-4116
              Sequence 158, Application US/08290665A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SW1
VCE 191 AA; 20766 MW; 182089 CN;
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 421792
INFORMATION FOR SEQ ID NO: 158:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: unknown
                                                                                                                                                                          NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.2%;
Best Local Similarity 89.9%;
Matches 98; Conservative
                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              umino acid
                                                                                                                                                                                                                                                                STATE: NEW YORK
                                                                                                                                                                                                                                               NEW YORK
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                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-290-665A-196
                                                                                                                                                                                                                                                                                                ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                                                         TITLE OF INVENTION: HCV-Specific Peptides, Agents Therefor TITLE OF INVENTION: and the Use Therof
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Pred. No. 2.01e-59;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/01/786,169A
FILING DATE: 19911031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filing Date:
Classification: 435
ATORNEY/AGENT INFORMATION:
NAME: Kirechner, Michael K.
REGISTRATION NUMBER: 34,851
REGISTRATION NUMBER: 02481-1118-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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JENCE 120 AA; 13619 MW; 70513 CN;
                                Sequence 6, Application US/07786169A GENERAL INFORMATION:
Sequence 6, Application US/07786169A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
                                                                                  APPLICANT: Stuber, Werner
APPLICANT: Gerken, Manfred
APPLICANT: Brust, Stefan
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
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Best Local Similarity 89.9%;
Matches 98; Conservative
                                                                      APPLICANT: Krupka, Udo
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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SEQUENCE Query Match ö

Gaps

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Indels

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Length 191;

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                                                                                   APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRTTRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.2%; Score 775; DB 45; Length 191; Best Local Similarity 89.9%; Pred. No. 2.01e-59; Matches 98; Conservative 2; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 AA.
                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FIOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/290, 665A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2026-4116
                                                       Sequence 196, Application US/08290665A
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                         Sequence 196, Application US/08290665A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 421792
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                      STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homosapiens INDIVIDUAL ISOLATE: Z7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                                                                                                                                                   STATE: NEW YORK
                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                    CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                               ZIP: 10154
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01-JAN-1900
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HEPATITIS C VIRUS (HCV) AND WHICH CAN BE USED ESP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                    Sequence 3, Application US/08380160
GENERAL INFORMATION:
APPLICANT: DALBON, Pascal
APPLICANT: JOLIVET, Michal
TITLE OF INVESTION: SYMTHETIC POLYPEPTIDES BELONGING TO THE
TITLE OF INVESTION: HEPATITIS C VIRUS (HCV) AND WHICH CAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 775; DB 54; Length 191; Pred. No. 2.01e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: FOR DETECTING THE LATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28682
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human Hepatitis C Virus VCE 191 AA; 20766 MW; 182089 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,471
FILING DATE: 05-WAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/380,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             Sequence 3, Application US/08380160
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OLIFF & BERRIDGE STREET: P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relephone: (703)836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VA
01-JAN-1900
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Feb 23-11:02

RESULT

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS: Sequence 159, Application US/08290665A GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. REGISTRATION NUMBER: 36,459 REFERENCE/DOCKET NUMBER: 2026-4116 TELECOMMUNICATION INFORMATION: APPLICATION NUMBER: US/08/290, 665A FILING DATE: 15-AUG-1994 CLASSIFICATION: 435 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: 191 AA; 20766 MW; 182089 CN; Sequence 159, Application US/08290665A. ADDRESSEE: MORCAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COMPUTER: IBM PC COMPATIBLE TELEX: 421792 INFORMATION FOR SEQ ID NO: 159: STANDARD; TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 ATTORNEY/AGENT INFORMATION: NAME: RICHARD W. BORK MEDIUM TYPE: FLOPPY DISK ORGANISM: homosapiens INDIVIDUAL ISOLATE: S18 LENGTH: 191 amino acids STRANDEDNESS: unknown SEQUENCE CHARACTERISTICS COMPUTER READABLE FORM: TOPOLOGY: unknown ORIGINAL SOURCE: TYPE: amino acid STATE: NEW YORK COUNTRY: USA US-08-290-665A-159 ZIP: 10154 01-JAN-1900 SEQUENCE XXXXXX

AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE CENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES 263 APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED PRT; REFERENCE/DOCKET NUMBER: 2026-4116 APPLICATION NUMBER: US/08/290, 665A FILING DATE: 15-AUG-1994 Sequence 160, Application US/08290665A Sequence 160, Application US/08290665A. COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE REGISTRATION NUMBER: 36,459 FELECOMMUNICATION INFORMATION: STANDARD; SOFTWARE: WORDPERFECT 5.1 TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 ATTORNEY/AGENT INFORMATION: LENGTH: 191 amino acids INDIVIDUAL ISOLATE: DR4 TELEX: 421792
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA: NAME: RICHARD W. BORK ORGANISM: homosapiens NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TOPOLOGY: unknown amino acid CITY: NEW YORK STATE: NEW YORK GENERAL INFORMATION: STRANDEDNESS: COUNTRY: USA ORIGINAL SOURCE US-08-290-665A-160 ZIP: 10154 01-JAN-1900 XXXXXX

99.2%; Score 775; DB 45; Length 191;

Query Match

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Gaps

; 0

Score 775; DB 45; Length 191; Pred. No. 2.01e-59; 2: Mismatches 9; Indels (

Query Match 99.2%; Best Local Similarity 89.9%; Matches 98; Conservative

191 AA; 20766 MW; 182089 CN;

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RESULT

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                                                                                                                      1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                   Gaps
                                                 ö
Score 775; DB 45; Length 191;
Pred. No. 2.01e-59;
                                                                                                                                                                                                                 61 RRQPIPKAXRXEGRSARAQPGYPWPLYGNEGCGMAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                           61 RRQPIPKARRPEGRTWAQPCYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                              9; Indels
                                                                                                                                                                                                                                                                                                                                       PRT; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.H.
NUCLEOTIDE AND DEDUCED
                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BURH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/290, 665A FILING DATE: 15-AUC-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 156, Application US/08290665A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 156, Application US/08290665A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 156:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
Query Match 99.2%;
Best Local Similarity 89.9%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rypE: amino acid
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SEQUENCE

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APPLICANT:

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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRCPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                           Length 200
                                                                                                                                                                                                                                                                                                                                       61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGP 109
                                                                                                                                                                                                                                                                                                                                                                    61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SUBESH M.
APPLICANT: DEVARE, SUSHIL G.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR ITILE OF INVENTION: PROTEINS
                                                                                                                                                                              9; Indels
LOCATION: 1..200
OTHER INFORMATION: /note= "HCV core protein, NYBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
                                                                                                                           Score 775; DB 38;
Pred. No. 2.01e-59;
                                                CHINFORMATION: isolate, see Fig. 5" 200 AA; 21771 MW; 201865 CN;
                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         1 MSTNPKPQRKTKRNTNRRPXXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: BCK, BILLY J.
APPLICANT: YAMAGUCHI, JULIE
APPLICANT: FRAIL, JULIE
APPLICANT: DESAI, SURESH M.
APPLICANT: DEVARE, SUSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                      Query Match 99.2%; Score 775; DB 58; Length 3011; Best Local Similarity 89.9%; Pred. No. 2.01e-59; Matches 98; Conservative 2; Mismatches 99; Indele n
                                                                                                                                                                                                                                                                                                                                                                                                    3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 3011 AA; 327108 MW; 47577590 CN;
                                                                                                      REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.US.01
                                      FILING DATE: APPLICATION NUMBER: US 07/830,024
                          APPLICATION NUMBER: US/08/144,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                         NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08710637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08710637.
                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                              FILING DATE: 01-JAN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-710-637-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1900
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 775; DB 68; Length 3011;
Pred. No. 2.01e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                     APPLICATION NUMBER: US 07/830,024
FILING DATE: 01-JAN-1992
ATYORNEY/AGENT INFORMATION:
NAME: POREMBEK!, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5131.US.01
                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
NENCE 3011 AA; 327194 MW; 47602524 CN;
                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,637
                                                                                                                 APPLICATION NUMBER: US/08/144,099
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                    LENGTH: 3011 amino acids
                                                                                                                                                                                                                               TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                          Watch 99.2%;
Local Similarity 89.9%;
                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                    98; Conservative
                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                              FILING DATE:
                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Search completed: Mon Feb 23 11:05:31 1998 Job time : 142 secs

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPerch pp

Mon Feb 23 11:02:22 1998; MasPar time 4.75 Seconds 486.554 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-836-075A-2 (1-109) from USO8836075A.pep 781 1 MSTNPKPQRKTKRNTNRRPX......GCGMAXWLLSPRGSRPNWGP 109 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Database:

Mean 39.606; Variance 82.455; scale 0.480 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred, No.	4.20e-127	4.05e-125	6.16e-123	9.72e-123	6.03e-122	6.03e-122	9.52e-122	3.74e-121	3.74e-121	8.70e-118	8.70e-118	8.70e-118	3.41e - 117
		9	ပ	ပ	ပ	ಲ	ပ	ဎ	ဗ	ပ	ပ	ပ္	ပ	ပ
	Description	SENOME POLYPROTEIN	SENC'ME POLYPROTEIN	ENOME POLYPROTEIN	SENOME POLYPROTEIN	_	SENOME POLYPROTEIN	GENOME POLYPROTEIN		SENOME POLYPROTEIN	SENOME POLYPROTEIN	ENOME POLYPROTEIN	SENOME POLYPROTEIN	ENOME POLYPROTEIN
	Des	19	ä	S	E	S	S	9	g	G	B	9	S	GE
	ID	POLG HCVH	POLG-HCV1	POLG HCVJA	POLG HCVJ2	POLG HCVJ7	POLC_HCVJ8	POLG HCVBK	POLG HCVH4	POLG HCVHK	POLG HCVJS	POLG HCVJT	POLG HCVJ6	POLC_HCVTW
	DB	_	^	-	-	-	٢	7	_	~	7	7	7	_
	luery Match Length DB	3011	3011	3010	513	737	3033	3010	520	520	737	3010	3033	3010
4°	Query Match	99.2	0.86	96.5	96.4	95.9	95.9	95.8	95.4	95.4	93.2	93.2	93.2	95.8
	Score	775	765	754	753	749	749	748	745	745	728	728	728	725
	Result No.	-	2	m	4	5	9	-	œ	6	10	11	12	13

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1.10e-02	2.05e - 02	6.95e - 02	1.71e-01	1.71e-01	2.30e-01	2.30e-01	2.30e-01	2.30e - 01	2.30e-01	3.08e-01	4.12e-01	4.12e-01	4.12e-01	5.51e-01	5.51e - 01	5.51e - 01	7.35e-01	9.79e - 01	9.79e-01	9.79e - 01	9.79e - 01	9.79e - 01	9.79e - 01	9.79e-01	1.30e+00	1.30e+00	1.30e+00	1.72e+00	1.72e+00	1.72e+00	2.28e+00
NONSTRUCTURAL POLYPRO	CCAAT DISPLACEMENT PR	BRAIN CALCIUM CHANNEL	ONCOSTATIN M PRECURSO	SON PROTEIN (SON3).	GTP CYCLOHYDROLASE I	PROTEIN-LYSINE 6-OXID	REGULATORY PROTEIN E2	RNA POLYMERASE BETA S	RNA POLYMERASE BETA S	ADENYLATE CYCLASE, TY	PROTEIN-LYSINE 6-0XID	REGULATORY PROTEIN E2	SUPPRESSOR OF WHITE A	SPERM PROTAMINE P1.	GTP CYCLOHYDROLASE I	UI SMALL NUCLEAR RIBO	LEUKOCYTE TYROSINE KI	SPERM PROTAMINE P1.	SPERM PROTAMINE P1.	SPERM PROTAMINE P1.	SPERM PROTAMINE P1.	GTP CYCLOHYDROLASE I	TRANSCRIPTIONAL REGUL	PEROXIDASE / CATALASE	VIRION INFECTIVITY FA	REGULATORY PROTEIN E2	NESTIN.		SPLICING FACTOR SC35	TRANSCRIPTIONAL REGUL	REGULATORY PROTEIN E2
POLN RUBVT	CDP CANFA	CB12 RABIT	OMCM BOVIN	SON HUMAN	GCH1 HUMAN	LYOX CHICK	VE2 HPV12	RRPI MEASE	RRPL MEASA	CYA5 CANFA	LYOX HUMAN	VE2 HPV20	SUWA DROME	HSP1_DASRO	GCH1 MOUSE	RU17 HUMAN	KLTK MOUSE	HSP1 DASVI	HSP1 SARHA	HSP1 TRIVU	HSP1 ANTSW	GCH1 RAT	IE63_EBV	CATA RHOCA	VIF HV2D2	VE2 HPV14	NEST HUMAN	H1L6 ENSMI	SC35 HUMAN	IE63_HSV11	VE2_HPV5B
-	7	7	7	6	4	9	10	œ	œ	n	9	10	6	2	4	6	S	ß	5	S	Ŋ	4	2	7	10	10	9	4	6	5	10
2205	975	2424	245	1523	250	420	494	2183	2183	1184	417	497	964	62	241	614	888	9	61	61	61	241	438	576	216	483	1618	101	221	512	514
13.3	13.1	12.5	12.2	12.2	12.0	12.0	12.0	12.0	12.0	11.9	11.8	11.8	11.8	11.7	11.7	11.7	11.5	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.3	11.3	11.3	11.1	11.1	11.1	11.0
104	102	86	92	95	94	94	94	94	94	93	92	92	95	91	91	91	90	89	83	88	68	68	68	68	88	88	88	8.1	8.1	87	98
14	15	16	11	18	19	20	21	22	23	24	22	56	27	88	53	30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Feb 23 10:59

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                                          CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C (POTENTIAL).
MAJORE ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/EZ (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/EZ (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OL-MG-1992 (REL. 28, LAST EXUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
PROTEIN (GNOTEIN (CONTRINS: CAPETION); MATRIX
PROTEIN (SNOTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2, NS44 AND NS48; HELICASE (NS3); RNA-DIRECTED RNA
POLYMERANSE (EC 2,7,1,48) (NS5).
HEPATITIS C VIRUS (ISOLATE 1) (HCV).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.

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REMOVED FROM CAPSID PROTEIN C BY THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                             HELICASE (NS3) (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (NS5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 775; DB 7; Length 3011;
Pred. No. 4.20e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 49643481 CRC32;
                                                                                                                                                                     POTENTIAL.
ATP (POTENTIAL).
DECH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                           (POTENTIAL).
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POLG HCVI STANDARD; | 1
P26654; | 01-AUG-1992 (REL. 23, CREATED)
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2041 2041
2240 2240
2364 2364
2789 2789
3011 AA; 327142 M
                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%;
89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Conservative
                                                                                                                                                                    369
1237
1319
                                                        115
191
383
729
1006
1615
1862
1862
2013
                                                                                                                                                                                                                             234
305
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423
430
448
476
532
532
556
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                  116
192
384
730
1007
1616
1863
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234
305
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532
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NP BIND
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2 2	FLAVIVIKUSES	555.	
2 2	SECTIENCE FROM N. A.	FROM N. A.	
X.	MEDLINE;	91172826.	
RA.	CH00 0L	CHOO QL., RICHMAN K.H., HAN J.H., BEI	RGER K., LEE
RA	GALLEGOS	C., COIT D., MEDIN	A-SELBY A., BARR P.J., WEINER A.J.,
æ	BRADLEY D	.W., KUO G., HOUGH	IJON M.;
H :	PROC. NAT	L. ACAD. SCI. U.S.	A. 88:2451-2455 (1991).
පු ද	-!- FUNCT	ION: THE SMALL PRO	-!- FUNCTION: THE SMALL PROTEINS NSZA, NSZB, NS4A AND NS4B ARE
ပ္ပ	HYDRO	PHOBIC, SUGGESTING	A POSSIBLE MEMBRANE-KELATED FUNCTION.
8	A SSN A	ND NS5 MAY PLAY A	
38	NOROS -:-	IT: THE VIKION OF	THIS VIKUS IS A NUCLEUCAPSID COVERED BY A
3	LIPOP	LIPOPROTEIN ENVELOPE. THE	KUILINS
သ	PROTE	IN M AND GLYCOPKO	PROTEIN M AND GLYCOPROTEIN E. THE NUCLEUCAPSID IS A CUMPLEX OF
ප	PROTE	IN C AND MRNA.	
DR	EMBL; M62	••	
DR	PIR; A39166;		
KW	POLYPROTEIN;	IN; GLYCOPROTEIN;	GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN;
K	COAT PROT	EIN; ENVELOPE PROT	COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
KW	NONSTRUCT	URAL PROTEIN.	
Ŀ	TNTT MET	-	REMOVED FROM CAPSID PROTEIN C BY THE
i ii		•	CELIII A AMINOPEPITO SE
7 E	M All	115	Cabeto poopets (Domewats)
-	CHAIN		MARRIX DECEMBER (POLEMIAL).
: E	CHAIN	101 303	
- E	CHAIN	192 383	PROIEIN E
H	CHAIN	•	NONSIRUCIORAL PROIETA NSI/EZ (POIENITAL).
<u>.</u>	CHAIN		
FT	CHAIN		
FT	CHAIN		NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
F	CHAIN	1863 2013	$\overline{}$
FT	CHAIN	2014 3011	RNA-DIRECTED RNA POLYMERASE (NS5)
FT			(POTENTIAL).
FI	TRANSMEM	m	
E.	NP BIND	1230 1237	ATP (POTENTIAL).
FT	SITE	1316 1319	DECH BOX.
FT	CARBOHYD	196 196	POTENTIAL.
FT	CARBOHYD	209 209	POTENTIAL.
Ē	CARBOHYD		POTENTIAL.
į.	CARBOHYD	305 305	POTENTIAL.
i E-	CARROHYD		POMENT 1A1.
. 6	CABBOUYD		DOMENT I A I.
4 6	dinogue,	624 624	
H	CAKBOHID		POIENITAL.
FT	CARBOHYD	4	POTENTIAL.
FI	CARBOHYD		POTENTIAL.
ĽЗ	CARBOHYD		POTENTIAL.
Ē	CARBOHYD	540 540	POTENTIAL.
Œ.	CARROHYD		POTENTIAL.
F	CARBOHYD	576 576	POTENTIAL.
F	CARBOHYD		POTENTIAL.
FT	CARROHYD		POTENTIAL.
i i	CARROHYD	~	POTENTIAL.
E L	CARROHYD		POTENT TAI.
: 5	CARROHYD		POTENTIAL.
e de	CARROHYD	2364 2364	POTENTIAL.
	CADDOUAN		DOMENTAL
. S	SEQUENCE	3011 AA; 327197	Σ
Ċ	Onerv Match	*0 86	Score 765: DB 7: Length 3011;
ж ф;	Best Local S	7	4.05e-125;
ΣÌ	Matches	96; Conservative	
qq	1 mstn 	mstnpkpqkknkrntnrrpqdv 	
οy	1 MSTN	PKPQRKTKRNTNRRPXX	mstnpkponktkrntnrrpxxxxxpggggivggvyllprrgprxgvratrktsersoprg 60

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ź					- E	CARBOHYD
2	61 rrqp1p.	karrpeg	irtwaqpgyp -	pwp.lygnegcgwagwllsprgsrpswgp 109	1 1	CARBOHYD
á	61 RRQPIP	KAXRXEG	RSWAQPGYPI	RRQPIPKAXRXEGRSWAQPGYPWDLYGNEGCGWAXWILSPRGSRPNWGP 109	: E	CARBOHYD
					FT	CARBOHYD
11000	,				FT	CARBOHYD
10027	010	CTA	CTANDAPD.	DBT: 3010 bb		CARROHYD
Ş.	P26662:	5	· mary		FT	CARBOHYD
DT	01-AUG-1992	(REL.	23. CREAT	(TED)	Ŀ	CARBOHYD
DI	01-AUG-1992	(REL.	23, LAST	(REL. 23. LAST SEQUENCE UPDATE)	F	CARBOHYD
DI	01-NOV-1995	(REL.	32, LAST	ANNOTATION UPDATE)	FT	CARBOHYD
핌	GENOME POLY	PROTEIN	(CONTAIN:	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX	ŏs	SEQUENCE
H.	PROTEIN (EW	VELOPE	PROTEIN M	PROTEIN (FNVELOPE PROTEIN M): MAJOR ENVELOPE PROTEIN E: NONSTRUCTURAL		
: :	PROTEINS NS	1. NS2.	NS4A AND	D NS4B: HELLCASE (NS3): RNA-DIRECTED RNA	õ	Ouery Match
1 E	POLYMERASE	(FC 2.7	7 48) (N	POLYWERASE (FC 2.7.48) (NS5)).	ĕ	Best Local Sin
2 2	HEDATITIS C	VIPIIS	(TSOLATE	HEDATITIS (VIBIS (1501at Japanese) (HCV)	×	Matches 97:
3 8	VIRIDAE: SS.	-RNA EN	VELOPED V	VIRIDAE: SS-RNA ENVEKOPED VIRISES: POSITIVE-STRAND: FLAVIVIRIDAE:		
8 8	HCV GROUP VIRUSES	TRUSES.			qQ	1 mstnp
RN	Ξ					·=
RP	SECUENCE FROM N.A.	OM N.A.			ò	1 MSTNPK
X.	MEDLINE; 91	91088550.			!	
æ	KATO N., HI	JIKATA	M., OOTSU	KATO N., HIJIKATA M., OOTSUYAMA Y., NAKAGANA M., OHKOSHI S.,	qq	61 rrqpip
æ	SUGIMURA T., SHIMOTOHNO K.;	, SHIMO	TOHNO K.;			Ξ
Æ	PROC. NATL.	ACAD.	SCI. U.S.	PROC. NATL. ACAD. SCI. U.S.A. 87:9524-9528(1990).	ργ	61 RRQPIE
S	[3]					
КР	SEQUENCE ANALYSIS.	ALYSIS.				
XX	MEDLINE; 91	91192160.			RESULT	JLT 4
RA	KATO N. HI	JIKATA	M. NAKAG	KATO N., HIJIKATA M., NAKAGAWA M., OOTSUYAMA Y., MURAISO K.,	a	POLG HCVJ2
RA	OHKOSHT S.	SHIMOT	OHNO K		AC	P27959;
	FEBS LETT, 280:325-328(1991).	280:325	-328 (1991		DI	01-AUG-1992
: :	-'- FUNCTIO	N: THE	SMALL PRO	FUNCTION: THE SMALL PROTEINS NS2B, NS2B, NS4B AND NS4B ARE	DT	01-AUG-1992
<u> ۲</u>	navauxn .	2 27 00	TICCESTING	O B DORGINE MEMBRANE DELINED EINCHION	T.	01-AHG-1992
3 5	NS3 AND	NS5 MA	V DIAY A	NIDACHODIC, JOGEDING R FOSIEDE FEMINANE FEMINE DE CONCILON. SA BAN NCS MAY DIAY A ROLF IN THE VIRAL RNA REPLIFORTION.	30	GENOME POLY
3 5	-1- STIBITALT	V 7HF V	TO NOT BY	THIS VIRIS IS A MICIEDCAPSID COURRED BY A	E	PROTEIN (EX
8 5	I TROPRO	TETN FN	VELOPE T		30	PROTEIN NS
3 5	PROTETN	MAND	GLYCOPROT	PROPERN M AND GLYCOPROTEIN F. THE NUCLEOCAPEON	00	HEPATITIS (
3 5	PROTEIN C AND MRNA	UNA C	MRNA		ဗ	VIRIDAE: SS
8 2	FMBI: D90208: G221611: -	8: 6221	611: -		ဗ	HCV GROUP V
8	PIR: A39253;	GNWVCJ.			RN	[1]
35	POLYPROTETN	GLYCO	PROTEIN	CONTINUE CITYCOPROTEIN: RNA-DIRECTED RNA POLYMERASE: CORE PROTEIN:	W W	SEQUENCE FF
3	COAT PROTEIN	N FNVE	TOPE PROT		RX XX	MEDLINE: 92
3	NONSTRUCTURAL PROTEIN	AI PROT	EIN.		R.	
	TNTT MET	-	-	REMOVED FROM CAPSID PROTEIN C RY THE	RA	TANAKA T
: 5	INIT THE	-	•	CELITIAN AMINODEPHIDASE	18	VIROLOGY 18
: 5	NIWIN	,	115	CADATA DECEMBER (POPENTIAL)	9	OLLUNIA TIT
: 5	CUNTN	116	101	MATERY DECEMBER (POTENTIAL)	3 5	HYDROPE
	CHAIN	193	383	MAJOR FRINTIONE DROPETIN F (POWENTAL)	3 2	NS3 AN
: 5	CHAIN		729	NONSTRICTION, DROTTIN NS1 (POTENTAL)	3 23	-!- SUBUNIT
	CHAIN	730	1006	NON-CTRICTIDAL DROPPIN NS (POTENTIAL)	9	1,TPOPRC
: 5	CHAIN		1615	HELICASE (NS3' (POTENTIAL).	88	PROTEIN
	CHAIN		1862	NONSTRICTIFAL PROTETN NS4A (POTENTIAL)	ຍ	PROTEIN
: 5	CUATN		2013	NONSTRIPTION DESCRIPTION NOAR (POPENTIAL)	DR	FMB1.: D1007
1 6	CHAIN	2014	3010	RANALDIRECTED RNA DOLYMERASE (NSS)	E. E.	POLYPROTEIN
: 5	Circin	F 107	200	(POTENTIAL)	X.	TRANSMEMBRA
: [-	TRANSMEM	347	369	POTENTIAL.	Ŀ.	INIT MET
F	NP BIND		1237	ATP (POTENTIAL).	FT	I
F	SITE		1319	DECH BOX.	FT	CHAIN
Ŀ	CARBOHYD	196	196	POTENTIAL.	En l	CHAIN
F	CARBOHYD	209	209	POTENTIAL.	E	CHAIN
E. 8	CARBOHYD	234	234	POTENTIAL.	1 L	TDANSMEM
c e	CARBOHYD	720	057	POTENTIAL.		CADDOUVD
	CARBOHID	500 714	203	POLENTAL	: E	CARBOHYD
-	CARBORLE	- 7	7	roteri iru.	:	

FT CARBOHYD 423 423 FT CARBOHYD 430 430 FT CARBOHYD 430 430 FT CARBOHYD 532 532 FT CARBOHYD 556 556 FT CARBOHYD 576 576 FT CARBOHYD 623 623 FT CARBOHYD 645 645 FT CARBOHYD 2041 2041 FT CARBOHYD 2041 2041 FT CARBOHYD 2077 2077 FT CARBOHYD 2788 2788 SQ SEQUENCE 3010 AA; 32701. QUETY MATCH 99.0\$; MATCHE 97; CORSELVATIVE DD 1 matnpkpqrktkrntnrpqdv MATCH 97; CORSELVATIVE DD 1 mstnpkpqrktkrntnrpqdv MATCH 111111111111111111111111111111111111	POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.	576 POTENTIAL. 623 POTENTIAL. 645 POTENTIAL. 041 POTENTIAL. 240 POTENTIAL. 788 POTENTIAL. 327017 MW; CZFZEG30 CRC32;	atch 96.5%; Score 754; DB 7; Length 3010; cal Similarity 89.0%; Pred. No. 6.166-123; 97; Conservative 2; Mismatches 10; Indels 0; Gaps 0; msthpkpqriktrntnrrpqdvkfpggqivgqvyllprrgprlqvratrktsersqprg 60
CARBG CARBG CARBG CARBG CARBG CARBG CARBG CARBG CARBG SEQUU 1		2 2 2 2 AA;	96.5%; Ilarity 89.0%; Conservative oqrkkrntnrrpqd
	CARBOHYD CARBOHYD CARBOHYD CARBOHYD	CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD	Query Matches Matches 1 1 61 61

RESULT ID P	ILT 4 POLG HCVJ2	STAN	STANDARD;	i,	PRT;	513 AA.	AA.					
AC DT	P27959; 01-AUG-1992	(REL. 2	23,	CREATED)	<u> </u>							
DI		(REL. 2	3,	LAST SI	(REL. 23, LAST SEQUENCE UPDATE)	PDAT	<u>a</u>					
L I	01-AUG-1992	(REL.	3,	LAST A	INOTATION			,				;
3 2	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN	ROTEIN		NIAINS	CAPSID	PROT	EIN	C (CORE	. K	TEIN	PROTEIN); MATKIX	Y 1 K
3 8	PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE FROTEIN PROTEIN NSI) (FRAGMENT).	ELOPE :	ENT	EIN 3).	MAJOK I	1	7 C	rkolen	3	CNON	X01.70X	2
S	HEPATITIS C VIRUS (ISOLATE HC-J2) (HCV).	VIRUS	(150	LATE HO	2-J2) (HC	3						
ဗ	VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;	RNA ENV	ÆL0	PED VI	RUSES; PC	SITI	VE-S	TRAND;	FLAV	IVIRI	JAE;	
ပ္ပ	HCV GROUP VIRUSES.	RUSES.										
Z.	[1]											
짪	SEQUENCE FROM N.A.	M N.A.										
RX	MEDLINE; 92230232.	30232.										
æ	OKAMOTO H., KURAI K., OKADA S.I., YAMAMOTO K., LIZUKA H.,	KURAI F	- ز	OKADA S	3.I., YA	AMOT	о Ж	, LIZUF	÷			
æ	TANAKA T., FUKUDA S., TSUDA F., MISHIRO S.;	UKUDA S	:	TSUDA I	F., MISH	IRO S	•÷					
R.	VIROLOGY 188:331-341 (1992).	:331-34	11	992).								
ပ္ပ	-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE	: THE S	MAL	L PROTI	EINS NS2	A, NS	2B, 1	NS4A AN	NS OF	4B ARI	r•3	
ပ္ပ	HYDROPHO	BIC, SU	JGGE	STING 1	HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.	불	MBRA	NE-REL		FUNCT	ION.	
ပ္ပ	NS3 AND	NS5 MAX	/ PL	AY A R(NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.	IE VI	RAL	RNA REI	LICA	TION.		
႘	-!- SUBUNIT:	THE VI	IRIO	N OF TH	SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY	S IS	A NU	CLEOCAL	SID	COVER		Æ
ပ္ပ	LIPOPROT	EIN EN	EIS	PE. THI	LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:	ă 8	NSIS	TS OF 1	윤	ROTEI	4S:	
႘	PROTEIN	M AND G	SLYC	OPROTE:	PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF	NIC	LEOC	APSID]	S A (COMPL	X OF	
ပ္ပ	PROTEIN C AND MRNA.	C AND N	ARNA									
DR	EMBL; D10074; G221589;	; G2215	589;	ï								
X	POLYPROTEIN; GLYCOPROTEIN; COAT PROTEIN; ENVELOPE PROTEIN;	GLYCOF	ROT	EIN; CC	DAT PROTE	IN;	ENVE	LOPE PI	OTEI	ž		
₹	TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.	E; NONS	STRU	CTURAL	PROTEIN.							
댎	INIT MET	-	-		REMOVED FROM CAPSID PROTEIN C	FROM	S	SID PRO	TEIN	C BY	THE	
FT	i				CELLULAR AMINOPEPTIDASE.	₩.	NOPE	PTIDASE	,.i			
F	CHAIN	7	115		CAPSID PROTEIN C (POTENTIAL) .	ROTE	INC	(POTE	TIAL	:		
FI	CHAIN	116	191		MATRIX PROTEIN (POTENTIAL)	ROTE	E N	POTENT]	IAL).			
FT	CHAIN	192	383		MAJOR ENVELOPE PROTEIN E (POTENTIAL)	WELD	표표	ROTEIN	E P	OTENT	IAL).	
FI	CHAIN	384 >	>513		NONSTRUCTURAL PROTEIN NS1	TURA	L PR	OTEIN !		POTEN	(POTENTIAL).	
FI	TRANSMEM		369		POTENTIAL.	ij.						
F	CARBOHYD	196	196		POTENTIAL.	Į.						
Ы	CARBOHYD	209	209		POTENTIAL.	ij.						

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	0; Gaps 0; reqprg 60	ISQPRG 60	PROTEIN); MATRIX E; NONSTRUCTURAL 'LAVIVIRIDAE; ILAVIVIRIDAE; NS4B ARE ED FUNCTION. 'LICATION. 'LICATION. 'LICATION. 'ST COWPLEX OF 'S A COMPLEX OF 'TEIN, 'TEIN, 'TEIN, 'TEIN, 'TEIN, 'TOTE (POTENTIAL). 'S (POTENTIAL). 'S (POTENTIAL).
POTENTIAL.	tch 96.4%; Score 753; DB 7; Length 513; al Similarity 89.0%; Pred. No. 9.72e-123; Indels 0; Gag; Conservative 2; Mismatches 10; Indels 0; Gagmentnpkpqrktkrntnrrpqdvkfpgggqivggvyllprrgprlgvratrktsersqprg	MSTNPKPQRKTKRNTNRRFXXXXXPGGGIVGGVYLLPRRGFRXGVRATRKTSERSQPRG 60 rrqpipkarrpegrawaqpgypwplygneglqwaqwllsprgsrpswgp 109	; 737 AA. CE UPDATE) TION UPDATE) SID PROTEIN C (CORE OR ENVELOPE PROTEIN (HCV) ; POSITIVE-STRAND; E ISHIRO S.; SIBLE MEMBRANE-RELAY SIBLE WEMBRANE-RELAY SIENCE CONSISTS OF TY THE NUCLEOCAPSID IN THE NUCLEOCAPSID IN WED FROM CAPSID PRO ULAR AMINOPETIDASE ID PROTEIN (POTENTIA THUCTURAL PROTEIN IN TRUCTURAL PROTEIN IN TRUTAL.
233 234 250 305 417 423 430 448 513	96.4%; arity 89.0%; Conservative	INTNRRPXXX rawaqpgyp : RSWAQPGYP	5 HUJJ STANDARD; GI, UG-1992 (REL. 23, CREATED) UG-1992 (REL. 23, LAST SER EINS NSI AND NS2) (FRACHES EINS NSI AND NS2) (FRACHES EINS NSI AND NS2) (FRACHES ENCE FROM N.A. INE; 92230232. OTO H., KURAI K., OKADA S., TSUDA F., FUKUDA S., TSUDA F., TSUDA F., TONDA S., TSUDA F.,
233 234 250 305 417 423 430 448 513 AA;	96.4 al Similarity 89.0 97; Conservativ mstnpkpqrktkrntnrr	KPQRKTKF pkarrpec PKAXRXEG	7 STANDARD 92 (REL. 23, C 92 (REL. 23, C 92 (REL. 23, L 92 (REL. 23, L 92 (REL. 23, L 92 (REL. 23, L 11YPROTEIN (CON ENVELOPE PROTE ENVELOPE PROTE ENVELOPE PROTE C VIRUS (ISOL SS-RNA ENVELOP VIRUSES. 92230232. 1, KURDA S., T 18 (18131-341(19) 10N: THE SMALL IND NSS MAY PLA IND SS MAY PLA IND GLYCOPEOTE IND MAND GLYCO IN C AND MRNA. 2 115 19 191 192 383 384 733 347 369 196 196 196 196 196 196 196 196 196 196 197 2219 197 373 173 737 173 737 174 737
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home/fuller/feb1098/US-08-836-075A-2.rsp	POTENTIAL.		86CAC08B											
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₩	305	417	423	4.30	448	477	534	542	558	578	627	649	737	737 AA;
Feb 23 10:59	CARBOHYD	NON TER	SEQUENCE											
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Gaps .**,** 61 rrqpipkdrrstgkswgkpgypwplygnegcgwagwllsprgsrptwgp 109 Indels 61 RRQP IPKAXRXEGRSWAQP GYPWPLYGNEGCGMAXWLLSPRGSRPNWGP 2; Mismatches 13; 94; Conservative Matches g ð ď

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DB 7; Length 737;

Score 749;

Pred. No. 6.03e-122;

86.2%; 95.98;

Best Local Similarity

Query Match

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GENOME POLYPROTEIN (CONTAINS: CAPEID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMEARSE (EC 2.7.7.48) (NS5); RNA-DIRECTED RNA HEDYMETIS C VIRUS (ISOLATE HC-J8) (HCV).
HEDATIS C VIRUS (ISOLATE HC-J8) (HCV).
HCV GROUP VIRUSES. 01-AUC-1992 (REL. 23, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE) PRT; 3033 AA. 01-AUG-1992 (REL. 23, CREATED) STANDARD; LT 6 POLG_HCVJ8 P26661; RESULT

[1] SEQUENCE FROM N.A.

OKRMOTO H., KURAI K., OKADA S.-I., YAMAMOTO K., LIZUKA H., TANAKA T., FUKUDA S., TSUDA F., MISHIRO S.; VIROLOGY 188:331-341(1992). MEDLINE; 92230232

HYDROPHOBIC, SUGGESTING NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN CAND MRNA.

EMBL; D10988 (221609). -.

PIR; A40250; GWWVJ8. POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.

CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL). 똺 REMOVED FROM CAPSID PROTEIN C BY CELLULAR AMINOPEPTIDASE. 115 191 383 INIT MET CHAIN CHAIN

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HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN BAVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MENA.

EMBI, MS835; G329711; -.

PIR, A88465; GNWYTC.

POLYPROTEIN; GLYCOPOTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/E2 (POTENTIAL). NONSTRUCTURAL PROTEIN NS48 (POTENTIAL) NONSTRUCTURAL PROTEIN NS48 (POTENTIAL) NONSTRUCTURAL PROTEIN NS2 (POTENTIAL). REMOVED FROM CAPSID PROTEIN C BY THE -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE Mome/fuller#eb1098/US-08-836-075A-2 rsp BOROWSKI P., HEILAND M., OEHLMANN K., BECKER B., KORNETEKY L.; EUR. J. BIOCHEM. 237:611-618(1996). RNA-DIRECTED RNA POLYMERASE (NSS) HELICASE (NS3) (POTENTIAL). CELLULAR AMINOPEPTIDASE. ATP (POTENTIAL). (POTENTIAL). POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL POTENTIAL. POTENTIAL POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL DECH BOX. 1615 1862 2013 3010 423 430 448 532 540 556 576 383 729 006 [2] SEQUENCE OF 1487-1500. MEDLINE; 96235224. 196 209 234 250 250 305 417 NONSTRUCTURAL PROTEIN. 1007 1616 1863 2014 423 430 448 Feb 23 10:59 TRANSMEM INIT MET CARBOHYD NP BIND CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN SITE

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Gaps

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2; Mismatches 11; Indels

Length 3010;

Score 748; DB 7; L Pred. No. 9.52e-122;

Query Match 95.8%; Best Local Similarity 88.1%;

96; Conservative

Matches

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327189 MW; 136A6A19 CRC32;

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61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109

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                                     01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1) (FRAGMENT).
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Pred. No. 3.74e-121;
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LAST ANNOTATION UPDATE)
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                                                                                                                    HEPATITIS C VIRUS (ISOLATE HCV-476)
                                                                                                                                                                                                 ABE K., INCHAUSPE G., FUJISAWA K.; J. GEN. VIROL. 73:2725-2729(1992). -!- SUBUNIT: THE VIRION OF THIS VII
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              STANDARD;
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01-JUL-1993
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RESULT 8
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AC Q01404;
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NONSTRUCTURAL PROTEIN NSI/E2 (FOTENTIAL).
BY SIMILARITY.
GENOME POLYPROTEIN (CONTAINS: CAFSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN A AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
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                                                                                        HEPATITIS C VIRUS (ISOLATE HCV-KF) (HCV).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
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VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
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POLYPROTEIN; GLYCOPROTEIN; COAT PROTEIN; ENVELOPE PROTEIN;
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Pred. No. 3.74e-121;
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01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
A ABE K., INCHAUSPE G., FUJISAWA K.;
L J. GEN. VIROL. 73:2725-2729(1992).
L J. THE VIROL OF THIS VIROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE; NONSTRUCTURAL PROTEIN.
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CARBOHYD
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REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NANSTRUCTURAL PROTEIN NSJ.E2 (POTENTIAL).
NONSTRUCTURAL PROTEIN NSJ.E2 (POTENTIAL). 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS N31, NS2, N34A AND NS48; HELICASE (NS3); RNA-DIRECTED RNA
POLYMERASE (EC 2.7.7.48) (NS5)). HYDROPHORE THE SMALL PROFEINS NS2B, NS2B, NS4B AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-!- SUBUNIT: THE VIRION OF THIS VIRAL RNA REPLICATION.

LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

PROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN CAND MRNA. 1 mstnpkpqrktkrntnrrpqdvkfpggggivggvyllprrgprlgvratrktsersqprg 60 Gaps ö 61 RRQPIPKAARXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWGP 109 EMBL; D10075; G221591; -. POLYPROTEIN; ENVELOPE PROTEIN; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN. 61 rrqpipkdrrstgkswgkpgypwplygneglgwagwllsprgsrpswgp 109 Score 728; DB 7; Length 737; Pred. No. 8.70e-118; OKAMOTO H., KURAI K., OKADA S.I., YAMAMOTO K., LIZUKA H., TANAKA T., FUKUDA S., TSUDA F., MISHIRO S.; VIROLOGY 188:331-341(1992). Indels 3; Mismatches 13; 737 81207 MW; 6AF1C5F4 CRC32; PRT; 3010 AA. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL POTENTIAL 93.2%; 85.3%; 93; Conservative STANDARD; 733 737 369 196 209 417 423 423 448 477 534 558 578 627 649 737 737 AA; Query Match Best Local Similarity MEDLINE; 92230232. 192 384 734 734 734 734 736 736 737 741 742 748 777 LT 11 POLG_HCVJT CARBOHYD CARBOHYD CARBOHYD CARBOHYD NON TER SEQUENCE CARBOHYD **TRANSMEM** INIT MET 000269; CHAIN CHAIN CHAIN CHAIN CHAIN Matches RESULT 1D PC AC QC DT 011 DT 011 DE GE DE PE DE PE 셤 셤 ò õ

88	HEPATITIS VIRIDAE;	C VIRUS SS-RNA EA	HEPATITIS C VIRUS (ISOLATE HC-JT) VIRIDAE; SS-RNA ENVELOPED VIRUSES	: C VIROS (ISOLATE HC-JT) (HCV). SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
8 8	HCV GROUP VIRUSES.	VIRUSES		
2	SEQUENCE FROM N.A.	FROM N.A.		
X X	TANAKA T.	72295/14 KATO N	NAKAGAW	A M OOTSUYAMA Y CHO M.J.,
S	NAKAZAWA	т., нілів	KATA M., I	NAKAZAWA T., HIJIKATA M., ISHIMURA Y., SHIMOTOHNO K.;
Z 5	VIRUS RES	. 23:39-: TON: THE	53(1992) SMALL DRO	FILMS NS
88	HYDROI	PHOBIC,	SUCCESTING	A POSSIBLE MEMBRANE-RELATED FUNCTION.
ខ	NS3 A	ND NS5 M	AY PLAY A	NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
3 8		ROTEIN EN	VIKION OF	<u> </u>
ខ	PROTE	IN M AND	PROTEIN M AND GLYCOPROTEIN E.	IN E. THE NUCLEOCAPSID IS A COMPLEX OF
ຮ	PROTE	IN C AND	MRNA.	
8 8	EMBL; D11168; G221613;	168; G22161 73: A45573	1613; 73	
¥ £	POLYPROTEIN;	IN; GLYCO	DPROTEIN;	
K	COAT PROTEIN;	EIN; ENV	ELOPE PROT	ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
X	NONSTRUCTURAL PROTEIN.	URAL PRO	rein.	THE NO S NIGHT DECK THE AND A STATE OF THE
<u></u> E	INIT	-	7	REMOVED FROM CAPSID FROIEIN C BI INE CELLITAR AMINOPEPTIDASE.
. [1	CHAIN	2	115	CAPSID PROTEIN C (POTENTIAL).
FT	CHAIN	116	191	MATRIX PROTEIN (POTENTIAL).
FT	CHAIN	192	383	MAJOR ENVELOPE PROTEIN E (POTENTIAL).
FT	CHAIN	384	729	NONSTRUCTURAL PROTEIN NSI/E2 (POTENTIAL)
1. 1.	CHAIN	1007	1615	NON-STRUCTURAL PROTEIN NSZ (POTENTIAL). HELLCASE (NS3) (POTENTIAL).
FT	CHAIN	1616	1862	PROTEIN NS4A (POTENTIAL)
FT	CHAIN	1863	2013	_
FT	CHAIN	2014	3010	RNA-DIRECTED RNA POLYMERASE (NS5).
	TRANSMEM	347	369	POTENTIAL.
. t	STE	1316	1319	
F	CARBOHYD	196	196	POTENTIAL.
FT	CARBOHYD	509	509	POTENTIAL.
FT	CARBOHYD	234	234	POTENTIAL.
FT	CARBOHYD	250	250	POTENTIAL.
1.6	CARBOHYD	505 417	303	POLENITAL.
- E	CARBOHYD	417	417	POTENTIAL.
FT	CARBOHYD	430	430	POTENTIAL.
FT	CARBOHYD	448	448	POTENTIAL.
E I	CARBOHYD	532	532	POTENTIAL.
. E	CARBOHYD	55.6	340 556	POIENTIAL
1 L	CARBOHYD	576	576	POTENTIAL.
FT	CARBOHYD	623	623	POTENTIAL.
FT	CARBOHYD	645	645	POTENTIAL.
FT	CARBOHYD	2041	2041	POTENTIAL.
FI	CARBOHYD	2011	2071	POTENTIAL.
1 6	CARBOHID	2529	2529	POTENTIAL.
1.3	CAPBOUND	9810	2788	POTENTIAL.
SQ.	SEQUENCE		AA; 326573	Σ
ā	/ Match	:	93.28;	Score 728; DB 7; Length 3010;
ďΣ	Best Local S. Matches 9	Similarity 94; Conse	í.	Pred. No. 8.70e-118; 3; Mismatches 12; Indels 0; Gaps 1
qū	1 mstn	pkpqrktk	rntyrrpqdv	(fpqqqqivqqvyvlprrgptlgvratrktsersqprg 60
			=	
δ	1 MSTN	PKPQRKTKI	RNTNRRPXXX	MSTNPKPORKTKRNTNRRPXXXXXPGGGOIVGGVYLLPRRGPRXGVRATRKTSERSOPRG 60

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558 558 POTENTIAL. 578 578 POTENTIAL. 649 649 POTENTIAL. 649 649 POTENTIAL. 1091 1091 POTENTIAL. 2038 2038 POTENTIAL. 2811 2811 POTENTIAL. 3033 AA; 329165 MM; 33355AC9 CRC32; Similarity 85.3%; Pred. No. 8.70e-118; 93.2% Conservative 3; Mismatches 13; Indels 0; Gaps 0;	mstnpkpqrktkrntnripqdvkfpgggivggvyllprigprlgvratrktsersqprg 60	T 13 PDLG HCVTW STANDARD; PRT; 3010 AA. P29846; 01-APR-1993 (REL. 25, CREATED) 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE) 01-APR-1994 (REL. 28, LAST ANNOTATION UPDATE) GENOME POLYROPTEIN (CONTAINS: CAPSID PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTROCTURAL PROTEINS NSI, NS2, NSA AND NS49; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)). HERATITIS C VIRUS (ISOLATE TAIMAN) (HCV). VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;	ENCE FROM N.A. INE; 92230206. 1P.J., LIN M.H., TAI K.F., LIU P.C., LIN C.J., CHEN D.S.; 1P.J., LIN M.H., TAI K.F., LIU P.C., LIN C.J., CHEN D.S.; LOCY 188:102-113(1992). FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NSS MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN G AND MENA. **, M8474; -, NOT_ANNOTATED_CDS.	Haj GANATAL. INJ. GIZCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; EIN, ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; URAL PROTEIN. REMOVED FROM CAPSID PROTEIN C BY THE CELLJILAR AMINOPEPTIOASE. 2 115 CORE PROTEIN (POTENTIAL). 116 191 MATRIX PROTEIN (POTENTIAL). 192 383 MAJOR ENVELOPE PROTEIN SOTENTIAL). 194 729 NONSTRUCTURAL PROTEIN NSJ/E2 (POTENTIAL). 1007 1615 HELICASE (NS3) (POTENTIAL). 116 1862 NONSTRUCTURAL PROTEIN NSJA (POTENTIAL). 11863 2013 NONSTRUCTURAL PROTEIN NSJA (POTENTIAL). 11863 2013 NONSTRUCTURAL PROTEIN NSJA (POTENTIAL). 11864 3010 RNA-DIRECTED RNA POLYMERASE (NSS). 1187 369 POTENTIAL.
0HYD 5 0HYD 5 0HYD 6 0HYD 10 0HYD 20 0HYD 28 6HYE 30 ENCE 30	mstnpkpqr 	T 13 POLG HCVTW ST POLG HCVTW ST 01-APR-1993 (REL. 01-APR-1993 (REL. 01-EEB-1994 (REL. GENOME POLYPROTEI PROTEIN (ENVELOPE PROTEIN (ENVELOPE PROTEINS (EC 2. HEPATITIS C VIRUS VIRIDAE, SS-RNA E HCV GROUP VIRUSES HCV GROUP VIRUSES	QUENCE FROM DILINE; 9223 EN P.J. II HYDROPHOE PROTEIN P PROTEIN P PROTEIN P PROTEIN P PROTEIN P	
FT CARB FT CARB FT CARB FT CARB FT CARB FT CARB SQ SEQUENT M Query M	90 63 69 63 64 65	RESULT 1D POLA 2D AC P 299 DT 01 DT 01 DT 01 DE PRO DE P		

CHAIN F ö Gaps ö Score 725; DB 7; Length 3010; Pred. No. 3.41e-117; 3; Mismatches 12; Indels 3010 AA; 327047 MW; 47E82A11 CRC32; (POTENTIAL) POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL. POTENTIAL POTENTIAL POTENTIAL POTENTIAL. POTENTIAL POTENTIAL. POTENTIAL POTENTIAL POTENTIAL POTENTIAL Query Match 92.8%; Best Local Similarity 86.2%; 94; Conservative 196 209 233 234 250 305 417 423 430 448 532 556 576 SITE CARBOHYD SEQUENCE

9 Matches 셤

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01-JAN-1990 (REL. 13, CREATED) 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE) 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE) NONSTRUCTURAL POLYPROTEIN (CONTAINS: NONSTRUCTURAL PROTEINS NSP1 TO RUBELLA VIRUS (STRAIN THERIEM). VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; TOGAVIRIDAE; PRT; 2205 AA DOMMINGUEZ G., WANG C.Y., FREY T.K.; VIROLOGY 177:225-258 (1990). SEQUENCE OF 1737-2205 FROM N.A. MEDLINE; 88226020. STANDARD; FREY T.K., MARR L.D.; GENE 62:85-99(1988). SEQUENCE FROM N.A. MEDLINE; 90281585. LT 14 POLN_RUBVT RUBIVIRUSES. P13889;

-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 EMBL; M15240; G333972; -.

NONSTRUCTURAL PROTEIN NSP1.

NONSTRUCTURAL PROTEIN.

PIR; A35320; MNWVRN. POLYPROTEIN; NONSTRUC

CHAIN ? ? NONSTRUCTURAL PROTEIN NSP3. CHAIN ? 2205 NONSTRUCTURAL PROTEIN NSP4. SEQUENCE 2205 AA; 240220 MM; E2158EB4 CRC32;	Query Match 13.3%; Score 104; DB 7; Length 2205; Best Local Similarity 33.3%; Pred. No. 1.10e-02; Matches 15; Conservative 13; Mismatches 14; Indels 3; Gaps 3;	613 aqargl-qafvrvvppperpwadggarawakffr-gcawaqrllg 655 : :: : : : 56 SQPRGRRQPIPKAXRXEGRSWAQPGY-PWPLYGNEGGGWAXWLLS 99	RESULT 15 TO CDP CANFA STANDARD; PRT; 975 AA.	1995 (REL. 31, CREAT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) CCART DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (PDAGMENTY)	(Francient). CUTLI OR CLOX. CANTE EMAITIABLE (PACE	CARIS FASTILIANIS (NOS). EKRAYOTA, METROAS, CHORDATA, VERTEBRATA, TETRAPODA; MAMMALIA; FIGURESTS, CABRITIODA		TISSUE-CARDIAC VENTRICULAR MUSCLE;	MEDLINE; 93161940. ANDRES V., NADAL-GINARD B., MAHDAVI V.;	DEVELOPMENT 116:321-334 (1992),	<u>!</u> .	MAY FUNCTION AS A DEVELOPMENTALLY REGULATED REPRESSOR OF TISSUE- SPECIFIC GENE TRANSCRIPTION BY PREVENTING THE INTERACTION OF		SEQUENCES, PROBABLY INVOLVED IN CELL-FATE SPECIFICATION IN DIVERSE DISCEPENDIAL DESCRIPTION DESCRIPTIO	4:			DETECTED MAINLY IN ADULT TISSUES AND TERMINALLY DIFFERENTIATED CELLS.	-!- SUBCELLULAR LOCATION: NUCLEAR.	-(- TISSUE SPECIFICITY: A BROAD PATTERN OF EARTESSION UBSERV TISSUES OF DIVERSE ORIGINS, SUCH AS CARTILAGE, LIVER, BR		THE LARGER ONE (250-220MD) IS FOUND MAINEL IN MODEL BRAIN, AND THE SMALLER ONE (180-190KD) PREDOMINATES IN	EMBRYONIC TISSUES,	-!- DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND	•	i 1		ALTERNATIVE SPLICING.	1.	MAMMALIAN COUNTERPART OF CUT. FAMR1: X69017: G2202: -	/
: E E S		da Ç	E 0 2	E T T	F 2 5	3 8 8	388	2 E 2	2	2 2	R.	88	8 8	88	ဗ ရ	38	8 8	38	ខខ	ဗ္ဗ (ខ្ល	ខ	38	ខ	ខ្ល	88	38	ខខ	ဗ	ខ្ល	ည္	5

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Query Match 13.1%; Score 102; DB 2; Length 975; Best Local Similarity 28.2%; Pred. No. 2.05e-02; Matches 20; Conservative 16; Mismatches 30; Indels 5; Gaps
R PIR; 533121; 533121.

R PROSITE; PSO0027; HOMEOBOX.

WH REDEAT; REPRESSOR; ALTERNATIVE SPLICING.

T NON TER 1 1 38 3 C. CUT. REPEATS.

T REPEAT C. 1 638 3 C. CUT. REPEAT.

T REPEAT 566 638 C. CUT. REPEAT.

T REPEAT 566 638 C. CUT. REPEAT.

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T REPEAT 567 C. CUT. REPEAT.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm

MPsrch nn

Run on:

Mon Feb 23 21:02:30 1998; MasPar time 235.86 Seconds 881.424 Million cell updates/sec

· Tabular output not generated.

>US-08-836-075A-1 (1-327) from USO8836075A.seq 317 Title:

Description: Perfect Score:

1 ATGAGCACGAATCCTAAACC.......CTCGGCCCAATTGGGGCCCC 327
TACTCGTGCTTAGGATTTGG.......GAGCCGGGTTAACCCCGGGG N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0

Nmatch STD:

1033316 seqs, 317879456 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-pending 1:PCT91 2:PCT92 3:PCT93 4:PCT94 5:PCT95 6:PCT95 7:PCT97 8:U75 9:U76 10:U7A 11:U7B 12:U78A 13:U78B 14:U79A 15:U78B 16:U800 17:U801 18:U802 19:U803 20:U804 21:U805 22:U806 23:U807 24:U808 25:U809 26:U810 27:U811 28:U812 29:U813 30:U814 31:U815 32:U816 33:U817 34:U818 35:U819 36:U820 37:U821 38:U822 39:U823 40:U824 41:U825 42:U826 43:U827 44:U828 45:U829 46:U830 47:U831 48:U832 49:U833 50:U834 51:U835 52:U836 53:UR77 54:U838 55:U839-56:U840 64:U848 65:U849 66:U85 67:U86 68:U87A 69:U87B 70:U87C 77:U6002A 78:U6002B 79:U6003A 80:U6003B 81:U6004A

Mean 8.813; Variance 3.802; scale 2.318 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match Length DB

No. Score

Result

Description

Pred. No.

886 896 896 896 896 496 316 146 146	14e-24 14e-24 14e-24 14e-24 14e-24 14e-24 14e-24 14e-24 14e-24 14e-23 82e-23 82e-23	20-6-73 8826-23 8826-23 8826-23 8826-23 8826-23 8826-23 8826-23 8826-23
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1, Ag 68, 1114, 1113, 5, Ag 1110, Ag 662, 7 662, 7 118, 7 1111, 11	25. 17. 17. 17. 17. 17. 17. 17. 17. 17. 17	1, 13, 13, 11, 13, 9, 9, 7, 7, 108, 108, 11, 11, 13, 13, 13, 13, 13, 14, 14, 14, 14, 14, 14, 14, 14, 14, 14
836- S -697- S -2290- S -2290- S -220- S -221- S -441- S -441- S -221- S -231- S -230- S -230- S	452-470-712-712-712-712-712-712-712-712-712-712	290- 290- 383- 384- 324- 324- 7169- 635- 635- 635- 635- 635- 635- 635- 635
7 87 US- 9 U	61 05- 63 05- 10 08- 110 08- 111 08- 113 08- 113 08- 81 08- 9 08- 9 08- 9 08- 854 08- 855 08- 856 08- 857 08-	45 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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317 305 285 285 283 283 282 282 282 281 281 281	281 281 281 281 281 281 281 281 279 279 279	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

ALI GNMENTS

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NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIA
             US-08-836-075A-1 STANDARD; DNA; UNC; 327 BP.
                                                       Sequence 1, Application US/08836075A Sequence 1, Application US/08836075A
                                                                                                   APPLICANT: MAERTENS, GEERT
                                                                                                                APPLICANT: STUYVER, LIEVEN
                                                                                                                              TITLE OF INVENTION:
                                                                                   GENERAL INFORMATION:
                                        01-JAN-1900
                             XXXXXX
RESULT
             CCCCCCEAGO
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AGENTS 207

TITLE OF INVENTION: NUMBER OF SEQUENCES:

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GNOSTIC

Feb 23 21:03

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGGCGACAGCCTATCCCCCAAGGCTCGYCGGYCCGAGGGCAGGTCCTGGGCTCAGCCCGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCGCCCTCAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCCCCCAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 317; DB 87; Length 327; 100.0%; Pred. No. 1.88e-275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 327 BP; 56 A; 102 C; 104 G; 51 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                  APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 oct 1995
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 oct 1994
                                                                                                                                                             APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
          ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 95870076.7
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                           FILING DATE: 28 Jun 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 327 base pairs
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
CORRESPONDENCE ADDRESS:
                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                            COUNTRY: USA
21P: 77210-4433
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                                     HOUSTON
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                                                   TEXAS
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Mome/fuller/feb1098/US-08-836-075A-1,rm Feb 23 21:03

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342 A.GAGCACGRATCCTAAACCYCAAARAARAAMCAAACGTAACACCAACCGYCGCCCACAG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 GACGTYAAGTTCCCGGCYGGYGGYCAGRTCGTTGGTGGAGTTTACYTGTTGCCGCGCAGG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGSCTNNNNNNCCGGGTGGCGGTCACATCGTTGGTGGAGTTTACCTGTTGCCGCGCGCAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 GGCCCYAGRITGGGTGTGCGCRCGACKAGRAAGACTTCCGAGCGGTCGCAACCTCGWGGW 521
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Pred. No. 1.07e-263;
                                                                                                                                                                                                                           TITLE OF INVENTION: POLYNUCLEOTIDE PROBES USEFUL FOR TITLE OF INVENTION: SCREENING FOR HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1645 BP; 229 A; 373 C; 384 G; 249 T; 410 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATORNEY ACENT INFORMATION:
NAME: Reed, Dianne E.
REGISTRATION NUMBER: 31,292
REFERENCE/DOCKET NUMBER: 2300-0207.00
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-327-7550
TELEFAX: 415-327-2951
                                                                      US-07-697-326A-68 STANDARD; DNA; UNC; 1645 BP
                                                                                                                                                                                                                                                                                                STREET: 545 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/697,326A
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               Sequence 68, Application US/07697326A
Sequence 68, Application US/07697326A
                                                                                                                                                                                                                                                                                    ADDRESSEE: Morrison & Foerster
301 CGCGCTCTCGGCCCAATTGGGCCCC 327
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                                                                                                                                                                                              APPLICANT: Kolberg, Janice
APPLICANT: Urdea, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1645 base pairs
                                                                                                                                                        APPLICANT: Cha, Tai-An
APPLICANT: Beall, Eileen
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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Local Similarity 80.1%;
Local Similarity 80.1%;
Local Similarity 80.1%;
                                                                                                                                                                                     Irvine, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19910508
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                       ZIP: 94025
                                                                                                                                                                                     APPLICANT:
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                                                                                                 01-JAN-1900
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### Application US/08290655A 1111111111111111111111111111111111	5																																			
26 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Feb 23 21:03 Atome/fuller/feb109&US-08-836-075A-1 mp		522 AGRCGWCARCCYATCCCYAAGGDCGYCRRCCCGAGGGYAGGRCCTGGGCYCAGCCYGGC	181 AGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCGAGG	582 TAYCCYTGCCCCTCTAYGCYAAYCAGGGY#KSGCRTGGGCRGGATGCTCTGTCMCCC	24. IAILCII IGGCCCC ICTATGGCAATGAGGGCTGCGGGTGGGCGGGGTTGGCTCCTGTCCCCC	301	100	SULT 3 SECTION STANDARD DAY INC. 573	03-00-250-005A-114 515MBARD, DRN, ORC, 515 XXXXX 01-13N-1900		GENERAL INFORMATION:	APPLICANT: BUKH, J., APPLICANT: PURCELL,	TITLE OF INVENTION:	TITLE OF INVENTION: TITLE OF INVENTION:	NUMBER OF SEQUENCES:	CORRESPONDENCE	STREET: 34		COUNTRY:		MEDIUM TYPE	OPERATING SYSTEM:	8	APPLICATION NUMBER:			REGISTRATION NUMBER: 36, 4	REFERENCE/DOCKET NUMBER: TELECOMMINICATION INFORMATIO		TELEX: 421792	INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:	LENGTH TYPE:	STRANI	OR	

ö GACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCGAGG 120 GGCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGA 180 181 AGGCGACAGCCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCCTCAGCCCGGG 240 9 241 TACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCC 300 APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. TITLE OF INVENTION: MICLEOTIDE AND DEDUCED TITLE OF INVENTION: AMINO ACID SQUEDICES OF THE ENVELOPE 1 AND TITLE OF INVENTION: CORE CENES OF ISOLATES OF HERATITIS C VIRUS TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES Gaps 1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCCCCACAG Acme/fuller/feb1098/IJS-08-836-075A-1.rmp ö Length 573; 4; Mismatches 26; Indels Sequence 573 BP; 98 A; 185 C; 177 G; 113 T; 0 other; Score 285; DB 45; Pred. No. 3.89e-244; US-08-290-665A-113 STANDARD; DNA; UNC; 573 BP CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/290, 665A Sequence 113, Application US/08290665A. Sequence 113, Application US/08290665A COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE SOFTWARE: WORDPERFECT 5.1 MEDIUM TYPE: FLOPPY DISK 89.9**%**; 90.8**%**; COUNTRY: USA ZIP: 10154 COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS: 297; Conservative NUMBER OF SEQUENCES: CITY: NEW YORK STATE: NEW YORK GENERAL INFORMATION: uery Match est Local Similarity 01-JAN-1900 23 21:03 XXXXXX tches 181

FILING DATE: 15-AUG-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK

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NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIA
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                                                                                                                                                                                                                                                                           Score 285; DB 45; Length 573;
Pred. No. 3.89e-244;
                                                                                                                                                                                                                                                                                                             4; Mismatches 26; Indels
                                                                                                                                                                                                             ORGANISM: homosapiens
INDIVIDUAL ISOLATE: P10
Sequence 573 BP; 96 A; 185 C; 179 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-836-075A-5 STANDARD; DNA; UNC; 327 BP.
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08836075A.
Sequence 5, Application US/08836075A
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CCCGCCTCTCGCCCCAATTGGGGCCCC 327
                                                                                             INFORMATION FOR SEQ ID NO: 113:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AGENTS
                                                                                                                             LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                            SEQUENCE CHARACTERISTICS:
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Best Local Similarity 90.8%;
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                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                               TOPOLOGY: linear ORIGINAL SOURCE:
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                                                                                TELEX: 421792
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181 AGGCGACAGCCTATTCCTAAGGCTCGCCAGTCCGATGGCAGNNCCTGGGCTCAGCCAGGG 240

61 GACGTCAAGNTCCCGGGTGGTGGTCAATCGTTGGTGGAGTTTACCTGTTGCCGCGCGAGG 120

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241 CATCCCTGGCCCCTCTATGGCAATGAGGGCTGCGGATGGCCGGGATGGCTCCTGTCCCCC 300

181

CGCGGCTCTCGGCCCAGTTGGGGCCCC 327 CCCCCTCTCCCCCAATTCCCCCCC 327

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CITY: HOUSTON

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Pred. No. 3.49e-242;
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                                                                                  SOFTWARE: Microsoft Word 6.0 / ASCII text output CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 327 BP; 62 A; 105 C; 103 G; 54 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches 27;
                                                                                                             APPLICATION NUMBER: US/08/836,075A FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/EP95/04155 FILING DATE: 23 Oct 1995
                                                                                                                                                                                                                                                             TORNET ALMERER, PATRICIA A.
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29, 775
                                                                                                                                                                                                                                APPLICATION NUMBER: EP 95870076.7 FILING DATE: 28 Jun 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          APPLICATION NUMBER: EP 94870166.9
                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                         FILING DATE: 21 Oct 1994 PRIOR APPLICATION DATA:
                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                       LENGTH: 327 base pairs
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity 90.5%;
Matches 296; Conservative
                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
            rry: USA
77210-4433
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181 AGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCCAGGTCCTGGGCTCAGCCCGGG 240
 121 GCCCCCAGGNNGGGTGTGCGCGCGACTAGGAAGACTTCCGAGGGGGTCACAACCTCGTGGC 180
                                                                                 241 CATCCTTGGCCCCTCTATGGCAATGAGGCCTTGGGGTGGGCAGGATGGCTCCTGTCACCC
                            GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS Version 3.3 SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/441,971 FILING DATE: 16-MAY-1995
                                                                                                                                                                                                                      US-08-441-971-62 STANDARD; DNA; UNC; 549 BP
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Wolf, Greenfield & Sacks, STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/221, 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
                                                                                                                                                                                                                                                              Sequence 62, Application US/08441971
Sequence 62, Application US/08441971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/697,326 FILING DATE: 8 May 1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                       301 cerecececeratreecece 327
                                                                                                                                                     301 CGCGCTCTCGGCCCAATTGGGGCCCC 327
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TELEFAX: (617) 720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 549 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCACAACCTCGTGGA 180
                                                                                                                      NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAGCACGAATCCTAAACCTCAAAGACAAACCAAACGTAACACCAACCGCCCCCCCACAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 89.3%; Score 283; DB 45; Length 573; Best Local Similarity 90.5%; Pred. No. 3.49e-242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 573 BP; 95 A; 189 C; 177 G; 112 T; 0 other;
            US-08-290-665A-110 STANDARD; DNA; UNC; 573 BP
                                                                                            APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/290,665A
                                                      Sequence 110, Application US/08290665A.
                                                                   Sequence 110, Application US/08290665A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY DISK COMPATIBLE COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                      TITLE OF INVENTION: NUCLEO: TITLE OF INVENTION: CARE OF TITLE OF INVENTION: AND THE TITLE OF INVENTION: SEQUENCES: 263
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: . single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homosapiens
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                  CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                         10154
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                                        01-JAN-1900
                              XXXXXX
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                                                                                                                                                                                                                                                       181 AGGCGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGCCAGGCCTGGGCTCAGCCCGGG 240
                                                                                                                                                                                                                                                                                                                   241 TATCCTTGGCCCCTCTATGGCAATGAGGGTCTGGGGTGGGCAGGATGGCTCCTGTCACCC 300
                                                                                                                                                                                                                                                                                                                                                                                          241 TATCCTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGNTGGCTCCTGTCCCCC 300
                                                                                                                   1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCCAACCGCCGCCCACAG 60
                                                                                                                                                 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCTCAK 60
                                                                                         Gaps
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0
                                                         Score 282; DB 60; Length 549;
Pred. No. 3.31e-241;
                                                                                       4; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
               INDIVIDUAL ISOLATE: spl
Sequence 549 BP; 92 A; 175 C; 173 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-221-653-62 STANDARD; DNA; UNC; 549 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/221,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/881,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/08221653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/08221653 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/697,326
                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGCCTCTCGGCCCAATTGGGGCCC 326
                                                                                                                                                                                                                                                                                                                                                                                                                        301 ccccccrcccccrAccrccccc 326
                                                                                                                                                                                                                                                                                                                                                                             STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URRENT APPLICATION DATA:
                                                          Query Match 89.0%;
Best Local Similarity 90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                      295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GACGTCAAGTTCCCGGGCGGTGGTCAATCGTTGGTGGAGTTTACCTGTTGCCGCGCGAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCCCCCAGGTTGGGTGTGCCCCCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAGGAGGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACACCGCCGCCCCAK 60
                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCGCCCACAG 60
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mome/fuller/feb1098/US-08-836-075A-1,rmp
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                                                                                                                                                                                                                                                                                                                                    Length 549;
                                                                                                                                                                                                                                                                                                                                                              4; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: spl Sequence 549 BP; 92 A; 175 C; 173 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  Score 282; DB 38; 1
Pred. No. 3.31e-241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-441-970-62 STANDARD; DNA; UNC; 549 BP
                                                                                               REFERENCE/DOCKET NUMBER: C0772/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 62, Application US/08441970.
Sequence 62, Application US/08441970
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCGGCTCTCGGCCTAGCTGGGGCCC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 cgcgcrcrcgcccAATTGGGCCC 326
                                                                 NAME: Janiuk, Anthony J. REGISTRATION NUMBER: 29,809
                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                      62:
                                                                                                                            TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    INFORMATION FOR SEC ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 549 nucleotides
                                       FILING DATE: 8 May 1991
                                                                                                                                                                                                                                                                                                                                  89.0%;
90.5%;
                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               295; Conservative
                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
                                                                                                                                                         TELEX: EZEKIEL
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1900
  Feb 23 21:03
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Massachusetts

COUNTRY:

Mome/fuller/feb1098/US-08-836-075A-1.mp

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FOR THE SIMULTANEOUS DIAGNOSIS OF HEPATITIS B AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.6%; Score 281; DB 87; Length 384; Best Local Similarity 90.5%; Pred. No. 3.14e-240; Matches 296; Conservative 3; Mismatches 28; Indels (
                                                                                                                      APPLICANT: Joong, Myung
APPLICANT: Choi, Deog Young
APPLICANT: Kim, Chun Hyung
APPLICANT: Kim, In Soo
APPLICANT: Kim, In Soo
APPLICANT: Choi, Dong Seob
TITLE OF INVENTION: DIAGNOSTIC KIT AND METHOD
TITLE OF INVENTION: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: KHCV CORE14, Fig. 1
Sequence 384 BP; 76 A; 120 C; 121 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 20,280
REFERENCE/DOCKET NUMBER: 8512-036-999
                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas
                  US-08-942-483-18 STANDARD; DNA; UNC; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/942,483 FILING DATE: 02-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,814
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: KR-93-7231
FILING DATE: 28-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jones III, Harry C.
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS LLP
                                                                   Sequence 18, Application US/08942483. Sequence 18, Application US/08942483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                        STATE: NY
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                                                    01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGGCGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGGCAGGTCCTGGGCTCAGCCCGGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GACGTCAAGTTCCCGGGCGGTGGTCAATCGTTGGTGCAGTTTACCTGTTGCCGCGCAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TATCCTTGGCCCCTCTATGGCAATGAGGGTCTGGGGTGGGCAGGATGGCTCCTGTCACCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAAACGCCGCCCACAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAGGAGAATCCTAAACCTCAAAGAAAACCAAACGTAACACAACCGCCGCCCTAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 549 BP; 92 A; 175 C; 173 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.0%; Score 282; DB 60; Best Local Similarity 90.5%; Pred. No. 3.31e-241;
                                               MEDIUM TYPE: Diskette, 5.25 inch COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS Version 3.3 SOFTMARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/441,970
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: C0772/7000
                                                                                                                                                                                                          APPLICATION NUMBER: 07/881,528
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 MAY 1991
ATTORNEY/AGET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGCTCTCGCCTAGCTGGGGCCC 326
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                                                                                                                                                                                                                                                                                                   NAME: Janiuk, Anthony J. REGISTRATION NUMBER: 29,809
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
                                                                                                                                                         FILING DATE: 16-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 549 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
   USA
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APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H. 301 ceceecreceecerActreeecece 327 301 ceceecrereecccAATTGGGCCCC 327 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE LENGTH: 384 base pairs TYPE: nucleic acid (212) 869-974 NUMBER OF SEQUENCES: 263 SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 88.68; al Similarity 90.5%; 296; Conservative STRANDEDNESS: single CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM nucleic acid TITLE OF INVENTION: TOPOLOGY: linear STATE: NEW YORK CITY: NEW YORK Local Similarity COUNTRY: USA ZIP: 10154 FEATURE: 01-JAN-1900 Query Match XXXXXX

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Db 121 121 181 181 181 181 181 181 181 181	61 GACGTCAACTTCCCGGCCCT 1 1 1 1 1 1 1 1 1	ADDRESSEE: ADGRAM & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: USA ZIP: 10154 COMPUTER: ELOPPY DISK COMPUTER: IND PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/290, 665A FILING DATE: 15-AUG-1994 CLASSIFICATION NUMBER: 36, 459 REFERENCE/DOCKET NUMBER: 36, 459 REFERENCE/DOCKET NUMBER: 36, 459 REFERENCE/DOCKET NUMBER: 36, 459 TELECHANNICATION NUMBER: 36, 459 REFERENCE/DOCKET NUMBER: 36, 459 TELECHANNICATION NUMBER: 36, 459 TELECHANNICATION NUMBER: 36, 459 TELECHANNICATION NUMBER: 36, 459 TELECHANNICATION POR SEQ ID NO: 115: SCOUTHANT CHARACTER.
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                                     ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T10
Sequence 573 BP; 99 A; 181 C; 176 G; 117 T; 0 other;
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Search completed: Mon Feb 23 21:06:34 1998 Job time : 244 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Feb 23 11:01:07 1998; MasPar time 7.41 Seconds 448.260 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-836-075A-2 (1-109) from US08836075A.pep 781

1 MSTNPKPQRKTKRNTNRRPX......GCGWAXWLLSPRGSRPNWGP 109 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unenc

Mean 38.341; Variance 95.496; scale 0.401 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 777 99.5 114 9 \$41366 genome polyprotein - 1 2 777 99.5 115 9 \$41364 genome polyprotein - 1 4 775 99.5 117 9 \$41364 genome polyprotein - 1 5 775 99.2 112 9 \$41341 genome polyprotein - 2 775 99.2 115 9 \$41345 genome polyprotein - 2 775 99.2 118 9 \$41345 genome polyprotein - 2 775 99.2 118 9 \$41345 genome polyprotein - 2 775 99.2 3011 4 GNWVCH genome polyprotein - 2 775 99.2 3011 4 GNWVCH genome polyprotein - 2 775 99.3 114 9 \$41365 genome polyprotein - 2 775 99.3 114 9 \$41365 genome polyprotein - 2 775 99.3 640 9 301364 genome polyprotein - 1 765 98.3 640 9 301584 genome polyprotein - 1 765 98.0 189 18 \$32740 core protein - hepat 1	Result No.	Score	Query Match	Query Match Length DB	03	10	Description	Pred. No.
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99.2 115 9 \$41345 99.2 118 9 \$41346 99.2 3011 4 GNWVCH 98.5 114 9 \$41365 98.5 114 9 \$41362 98.3 640 9 JQ1584 98.0 189 18 \$32740	4	775	99.5		9	541341	genome polyprotein -	2.23e-106
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1.03e-104	2.21e-104	3.23e - 104	6.90e-103	6.90e - 103	1.01e-102	1.48e - 102	2.17e-102	2.17e-102	4.67e-102	4.67e-102	4.67e-102	6.84e-102	1.00e-101	1.00e-101	1.47e-101		2.15e - 101	2.15e-101	2.15e-101	3.16e-101	3.16e-101	3.16e-101	3.16e - 101	63e-	6.78e-101	3.13e - 100	6.71e-100	9.84e - 100	9.84e - 100	1.44e - 99	1.44e - 99	1.44e - 99	1.44e - 99
genome polyprotein -	polyprotein precurso	genome polyprotein -	hypothetical protein	polyprotein - hepati		genome polyprotein -	hypothetical protein	genome polyprotein -	genome polyprotein N	genome polyprotein -	structural protein -	genome polyprotein -	polypeptide - hepati																				
GNWVC3	240770	S41344	S41343	GNWVCJ	S12707	S41359	S41342	\$41360	S41361	JQ0883	GNWVJ8	GNWVTC	541347	541351	PC1284	JQ1925	JQ1926	S18031	PN0677	S41358	PC2061	541288	A44150	JH0711	S41368	S19876	541367	JN0265	S21471	541371	S41370	S41350	PC2219
4	2	σ	9	4	6	6	6	6	6	6	4	4	6	6	6	6	6	6	6	6	6	9	9	9	6	σ	6	6	6	9	6	6	9
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0.86	7.76	97.6	96.5	96.5	96.4	96.3	96.2	96.2	95.9	95.9	95.9	95.8	92.6	92.6	95.5	95.4	95.4	95.4	95.4	95.3	95.3	95.3	95.3	95.1	95.0	94.5	94.2	94.1	94.1	94.0	94.0	94.0	94.0
765	163	762	754	754	753	752	751	751	749	749	749	748	747	747	746	745	745	745	745	744	744	744	744	743	742	738	736	735	735	734	734	734	734
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ALI GNMENTS

	S41366 #type fragment	genome polyprotein - hepatitis C virus (genotype 4, N5)	(fragment)	core protein	#formal name hepatitis C virus	genotype 4, N5	19-May-1994 #sequence revision 26-Jul-1996 #text_change	16-Feb-1997	\$41366	541341	van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.	submitted to the EMBL Data Library, January 1994	Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.	541366	##molecule type genomic RNA	1-114 ##label VAN	##cross-references EMBL: 229469	##experimental source genotype 4, N5	#superfamily hepatitis C virus genome polyprotein	capsid protein; core protein; polyprotein		#product core protein #status predicted #label MAT	#length 114 #checksum 8901
RESULT 1	ENTRY	TITLE		CONTAINS	ORGANISM	#variety	DATE		ACCESSIONS	REFERENCE	#authors	#submission	#description	#accession	##molecnl	##residues	##cross-r	. ##experim	CLASSIFICATION	KEYWORDS	FEATURE	1-114	SUMMARY

99.5%; Score 777; DB 9; Length 114;

Query Match

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genotype 4, N3
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#length 115 #checksum 8983
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genome polyprotein - hepatitis C virus (genotype 4, N3)
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Pred. No. 1.04-106;
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Best Local Similarity 90.8%;
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19-May-1994 #sequence_revision 26-Jul-1996 #text_change
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#length 112 #checksum 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
841341
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##cross-references EMBL:229444
##experimental_source genotypel, NI
FEXTORION #superfamily hepatitis C virus genome polyprotein
                                                                            ##experimental_source genotype 4, N2
FICATION #superfamily hepatitis C virus genome polyprotein
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Pred. No. 2.23e-106;
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                                  ##residues 1-117 ##label VAN ##cross-references EMBL:Z29466
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                   ##molecule_type genomic RNA
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TITLE genome polyprotein - hepatitis C virus (genotype 1, N3)	
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<pre>#Variery genocype 1, ns 19-May-1994 4 sequence_revision 26-Jul-1996 #text_change 16.Eb.1007</pre>	QO
ACCESSIONS \$41345 PREPRINCE \$41341	Qy
van D submi Analy S4134	RESUL' ENTRY TITLE CONTA
#fresidues 1-115 #flabel VAN #fcross-references EMBL:229448 #fexperimental source genotype 1, N3 CLASSIFICATION #superfamily hepatitis C virus genome polyprotein CEXYMORDS capsid protein; core protein; polyprotein	ORGAN #n
<pre>#product core protein fstatus predicted flabel MAT #length 115 fchecksum 9357</pre>	ACCES
Query Match 99.2%; Score 775; DB 3; Length 115; Best Local Similarity 89.9%; Pred. No. 2.23e-106; Matches 98; Conservative 2; Mismatches 9; Indels 0; Gaps 0;	त्य छ्वाच्या स्थाप
1 mstnpkpgrktkrntnrrpgdvkfpggggivggvyllprrgprigvratrktsersgprg 60 	j αj ∗ •••
61 rrqpipkarrpegrtwaqpgypwplygnegcgwagwllsprgsrpswgp 109 	REFERI
S41346 #type fragment genotype 1, N4)	eer eer
*	# # # # # # # # # # # # # # # # # # #
ACCESSIONS \$41346 REFERENCE \$41341 Fauthors van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T. #submission submitted to the EMBL Data Library, January 1994 #description Analysis of hepatitis C virus genotypes 1 to 5 by LiPA. #accession \$41346	FEATU 1- 11 19
##molecule_type_genomic_RNA #fresidues 1-118 #flabel VAN #fresidues 1-118 #flabel VAN #fresidues EMBL:23449 #fexperimental source genotype 1, N4 CLASSIFICATION #superfamily hepatitis C virus genome polyprotein capsid protein; core protein; polyprotein	39 73 10
<pre>#product core protein fstatus predicted flabel MAT flength 118 fchecksum 81</pre>	16
Query Match 99.2%; Score 775; DB 9; Length 118; Best Local Simitarity 89.9%; Pred. No. 2.23e-106; Matches 98; Conservative 2; Mismatches 9; Indels 0; Gaps 0;	20 20

Db 1		mstnpkpgrktkrutnrrpqdvkfpgggqivggvylprrgprlgvratrktsersqprg 60
Qy 1		ORKTERNTNRRPXXXXXXPGGGQIVGGVYLLERRGPRXGVRATRKTSERSQPRG 60
Db 61		rrqpipkarrpegrtwaqpgypwplygnegcqwagwllsprgsrpswgp 109
Qy 61		CAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
RESULT	7	
ENTRY		GNWVCH ftype complete
CONTAINS		capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NSI; nonstructural protein NSI; nonstructural protein NSI;
		nonstructural protein NS4b; nonstructural protein NS5
ORGANISM		#formal_name hepatitis C virus
#note DATE		host Homo sapiens (man) 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
PNOTPRESCO		16-Feb-1997 n 36814: n 41546
REFERENCE		
#authors	ırs	Inchauspe, 6.; Zebedee, 5.; Lee, D.H.; Sugitani, M.; Nasoii, M.; Prince, A.M.
#submi	submission	d to GenBank, July 1992
#desci	description	Genomic structure of the human prototype strain H of hepatitis C virus: comparison with American and Japanese
		ates.
#accession	ssion	A35814 + gonomic DNA
* *	##molecule_Lype ##residues	LYPE GENOMIC ANA 1-3011 ##label INC
D##	ross-re	##cross-references GB:M67463
AEFERENCE	ır.	A41340 Inchauspe. G.: Zebedee. S.: Lee. D.H.: Sugitani, M.: Nasoff,
	2	e, A.M.
# journal	la!	Proc. Natl. Acad. Sci. U.S.A. (1991) 88:10292-10296
*		
4	j	isolates.
#Cross-re	-reierel	#Cross-reletences Mulu:92032236 #contents annotation
#note		neither amino acid nor nucleotide sequence is given
CLASSIFICATION KEYWORDS	ATION	#superfamily hepatitis C virus genome polyprotein capsid protein; envelope protein; qlycoprotein; nonstructural
FEATURE		protein; polyprotein; transmembrane protein
1-115		#product capsid protein C #status predicted #label CPC\
116-191	11	
192-38	68	٠ زړ
390-72	6	<pre>#label MEE.\ #product nonstructural protein NS1 #status predicted</pre>
000	5	NS1\
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1007-161	(615	<pre>#product nonstructural protein NS3 #status predicted #label NS3</pre>
1616-1862	862	
1863-201	1013	
2014-3011	3011	
		#label NS5\

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CONTAINS 임 à 셤 õ ö ö 1 mstnpkpgrktkrntnrrpqdvkfpggggivggvyllprrgprlgvratrktsersqprg 60 #binding_site carbohydrate (Asn) (covalent) #status 1 mstnpkpqrktkrntnrrpmdvkfpgggqivggvyllprrgprlgvratrktsersqprg 60 Gaps Gaps 19-May-1994 #sequence_revision 26-Jul-1996 #text_change *product core protein *status predicted *label MAT genome polyprotein - hepatitis C virus (genotype 4, N4) genome polyprotein - hepatitis C virus (genotype 4, N1) by LiPA predicted #length 3011 #molecular-weight 327143 #checksum 438 0, .; 0 submitted to the EMBL Data Library, January 1994 Analysis of hepatitis C virus genotypes 1 to 5 by S41365. Query Match 99.2%; Score 775; DB 4; Length 3011; Best Local Similarity 89.9%; Pred. No. 2.23e-106; 98.5%; Score 769; DB 9; Length 114; 89.9%; Pred. No. 2.22e-105; van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T. 9; Indels 9; Indels capsid protein; core protein; polyprotein 2; Mismatches 2; Mismatches fformal_name hepatitis C virus #length 114 #checksum 8888 #type fragment #type fragment 1-114 ##label VAN ##cross-references EMBL:229468 #molecule_type genomic RNA Best Local Similarity 89.9%; genotype 4, N4 98; Conservative 16-Feb-1997 98; Conservative core protein (fragment) \$41365 \$41341 196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2240, 2364, 2789 #fresidues description CLASSIFICATION submission #accession Query Match œ 6 fvariety #authors ACCESS IONS 19 Matches Matches REFERENCE 1 - 114CONTAINS ORGANISM KEYWORDS SUMMARY SUMMARY FEATURE RESULT ENTRY TITLE RESULT TITLE DATE 셤 ð g õ g g ð Š

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ö expression of putative core gene of hepatitis C virus from *superfamily hepatitis C virus genome polyprotein core protein; envelope protein; glycoprotein; nonstructural fproduct envelope protein E2 and nonstructural protein product core protein C #status predicted #label CPC\ product envelope protein El #status predicted #label E2; 9 Gaps #formal name hepatitis C virus
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
03-May-1994 genotype 4, N1 19-May-1994 #sequence_revision 26-Jul-1996 #text_change Analysis of hepatitis C virus genotypes 1 to 5 by LiPA. \$41362 core protein C; envelope protein E1; envelope protein nonstructural protein NS1 1 mstnpkpqrktkrntnrrpmdvkfpgggqivgglyglprrgprlgvratrktsersqprg genome polyprotein - hepatitis C virus (strain U.K.) Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J. J. Gen. Virol. (1992) 73:1521-1525 Cloning and sequencing of the structural region and ö ##experimental source genotype 4, N1 CLASSIFICATION #superfamily hepatitis C virus genome polyprotein van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T. submitted to the EMBL Data Library, January 1994 a British case of chronic sporadic hepatitis. Length 114, Indels 61 RROPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP capsid protein; core protein; polyprotein NS1 #status predicted #label EE2\ 6 Score 769; DB 9; LA Pred. No. 2.22e-105; 2; Mismatches formal name hepatitis C virus #type fragment ##residues 1-114 ##label VAN ##cross-references EMBL:Z29465 1-640 ##label KUM protein; polyprotein ##molecule_type genomic RNA ##molecule_type genomic RNA Query Match Best Local Similarity 89.9%; 98; Conservative 16-Feb-1997 core protein 띮 JQ1584 JQ1584 JQ1584 S41362 \$41341 JQ1584 #fresidues description submission CLASSIFICATION #accession 2 authors authors | variety journal ACCESSIONS 192-389 390-640 ACCESSIONS Matches REFERENCE REFERENCE title 1 - 114[-191 ORGANISM KEYWORDS CONTAINS ORGANISM KEYWORDS FEATURE SUMMARY FEATURE RESULT TITLE ENTRY

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Analysis of a new hepatitis C virus type and its phylogenetic capsid protein; envelope protein; glycoprotein; nonstructural ö #product capsid protein C #status predicted #label CPC\
#product envelope protein M #status predicted #label nonstructural protein NS4a #status predicted nonstructural protein NS4b #status predicted Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L.; Simmonds, P. J. Gen. Virol. (1992) 73:1131-1141 nonstructural protein NS3 #status predicted nonstructural protein NS5 #status predicted 9 #binding_site carbohydrate (Asn) (covalent) #status Gaps #length 3011 #molecular-weight 327199 #checksum 8610 1 mstnpkpqkknkrntnrrpqdvkfpggggivggvyllprrgprlgvratrktsersqprg ö #superfamily hepatitis C virus genome polyprotein nonstructural protein NS1 #status nonstructural protein NS2 #status Score 765; DB 4; Length 3011; Pred. No. 1.03e-104; major envelope protein E #status protein; polyprotein; transmembrane protein Indels 3; Mismatches 10; relationship to existing variants. ##molecule_type genomic RNA ##residues 1577-1633 ##label CHA ##status preliminary ##molecule_type genomic RNA ##residues 1577-1633 ##label CH2 #fexperimental source isolates E-b16 cession PQ0404 ##experimental source isolates E-b17 **Iesidues 1-3011 ##label CHO
##cross-references GB:M62321
NCE. #cross-references DDBJ:D10128 NS1/ NS3/ MEE NS2 predicted Query Match 98.0%; Best Local Similarity 88.1%; product #label #label #label product product #label #label product #label #product #product #product 96; Conservative #label EPM\ ##molecule_type mRNA P00403 PQ0393 196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 2240, 2364, 2550, 2789 CLASSIFICATION accession *accession 1007-1615 1616-1862 1863-2013 2014-3011 #authors # journal 730-1006 390-729 192 - 389116-191 REFERENCE title Matches 1-115

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#checksum 9764

#length 115

ö ö 9 S41343 ftype fragment genome polyprotein - hepatitis C virus (genotype 1, N11) Gaps Gaps genotype 1, N11 19-May-1994 #sequence revision 26-Jul-1996 #text_change van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T. submitted to the EMBL Data Library, January 1994 Analysis of hepatitis C virus genotypes 1 to 5 by LiPA. #product core protein #status predicted #label MAT 1 mstnpkpgrktkrntnrrpgdvkfpggggivggvylwprrgprlgvratrktsersqprg ö ö fexperimental source genotype 1, N11
ICATION fsuperfamily hepatitis C virus genome polyprotein Score 762; DB 9; Length 115; Pred. No. 3.23e-104; 96.5%; Score 754; DB 9; Length 115; 89.0%; Pred. No. 6.90e-103; Indels Indels capsid protein; core protein; polyprotein 2; Mismatches 10; 2; Mismatches 10; |formal_name hepatitis C virus #length 115 #checksum 9697 Search completed: Mon Feb 23 11:02:03 1998 1-115 ##label VAN ##cross-references EMBL: 229446 ##molecule_type genomic RNA Query Match 97.6%; Best Local Similarity 89.0%; Best Local Similarity 89.0%; 97; Conservative 97; Conservative 16-Feb-1997 core protein (fragment) S41343 S41341 S41343

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn MasPar time 435.69 Seconds 106C.033 Million cell updates/sec Mon Feb 23 20:43:03 1998; Run on:

Tabular output not generated.

(1-327) from USO8836075A.seq 317 >US-08-836-075A-1 Title:

Description: Perfect Score: N.A. Sequence:

1 ATGAGCACGAATCCTAAACC.....CTCGGCCCAATTGGGCCCCC 327 TACTCGTGCTTAGGATTTGG......GAGCCGGGTTAACCCCGGG

TABLE default Scoring table:

Gap 6

430261 seqs, 710217276 bases x 2 Searched:

Dbase 0; Query 0

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-new7 Database:

1:BCT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HUM1 9:HUM2 10:HUM3 11:INV1 12:INV2 13:ORC 14:MAM 15:VRT 16:PLN 17:PRO1 18:PRO2 19:ROD 20:SYN 21:UNC 22:VIR

genbanka 101

Database:

23.671 24.18CT2 25.8CT3 26.8CT4 27.8CT5 28.8CT6 29.8CT7 30.8CT8 31.8CT9 32.8CT10 33.8CT11 34.8CT12 35.8CT13 35.6CN1 37.6CN2 38.6CN3 39.6CN3 41.8CT12 35.8CT13 35.6CN3 41.8CN5 41.6CN6 41.8CN5 41.8CN5 41.8CN5 41.8CN5 41.8CN5 41.8CN5 41.8CN5 41.8CN1 48.1RV2 49.1RV1 57.1RV4 51.1RV5 52.1RV6 53.1RV7 54.1RV8 55.1RV9 56.1RV9 57.1RV1 58.1RV12 59.8MAN 60.8MAN 63.VRT2 64.VRT3 65.VRT4 66.PAT1 67.PAT2 68.PAT3 69.PAT4 70.PAT5 71.PAT6 72.PAT7 73.PHG 74.PLN1 75.PLN2 76.PLN3 77.PLN4 78.PLN5 79.PLN6 80.PLN7 81.PLN8 82.PLN9 83.PLN10 84.PLN1 85.PLN12 86.PR11 87.PR12 88.PR13 89.PR14 90.PRIS 91.PRIG 92.PRIT 93.PRIB 94.PRI9 95.PRI10 96.PRII1 97.PRII2 98.PRII3 99.PRII4 100.PRII5 101.PRII6 102.PRIIT 103.RODI 104.RODZ 105.RODZ 106.RODZ 107.RODZ 108.RODG 109.RODT 110.RODZ 111.RODZ 112.STR 113.SYN

115;VRLJ 116;VRL2 117;VRL3 118;VRL4 119;VRL5 120;VRL6 121;VRL7 122;VRL8 123;VRL9 124;VRL10 125;VRL31

Natabase:

genbank-new7 126:BCT 127:GEN 128:HTG1 129:HTG2 130:INV 131:MAM

Database:

home/fuller/feb1098/US-08-836-075A-1 rge Feb 23 20:47 138:ROP 139:SYN 140:UNA 141:VRL

u-emb151 101

Database:

142:part1 143:part2

Mean 9.880; Variance 4.750; scale 2.080

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.		ė		7.81e-216	7.81e - 216	7.81e-216	7.81e-216	7.81e-216	,81e-	.84e-	4.36e-214	4.36e-214	•	.36e-	.36e-	.36e-	.36e-	. 26e-	. 26e-	. 26e-2	4.	₹.	₹.	4.	2.43e - 212	2.43e-212	2.43e-212	2.43e - 212	2.43e-212	2.43e-212	2.43e-212	2.43e-212	2.43e-212	2.43e-212	2.43e	2.43e-212	43e-212	.43e-	.43e-	2.43e-	2.43e -	2.43e-	1.82e-	1.82e-	1.82	1.82e-211
		from Paten	virus cor	virus iso	virus iso		-	virus (st		Vir	from Paten	virus (ge	virus iso	virus (HC		virus (st	virus str	virus gen	virus gen	virus gen		virus cor	virus iso				virus cor	e encodin	virus	virus		g a part		chimp		peptide	lepatit	virus	-	[Hepat		virus	-		virue	9 from Pate
Description		Sequence 1	Hepatitis C	Hepatitis C	Hepatitis C	~		Hepatitis C		Hepatitis C	S	Hepatitis C		Hepatitis C				cDNA to 5'-t	cDNA encoding	Hepatitis C	DNA encoding	ET.	Hepatitis C	Hepatitis C	polyprotein	Hepatitis C	Hepatitis C	Hepatitis (Hepatitis (00	Sequence 45															
I QI		A50346	HCVHN3	HCU10204	HCU10193		HPCCGENOM	HPCK1S1	HPCK1R1	HPCNS1SPC	A50350	HCVCR1N5	HCU10209	нРСИС32	HPCK1R2	HPCK152	HPCJRNA	HPCHCV006	HPCHCV007	D85516	HCVHB1	HCVHN2	HCU10225	HCU10203	HCU10189	HCU10202	HCU63376	E03572	HPCSTRUCTB	HPCE2COR	HPC5TRJ4	E04260	E04805	E07391	HPCPOLYPRO	E04421	E07579	HPCUNKCDS	HCU16362	s62220	HPCJ483	HPCRNA	HPCHCV010	HPCHG2F	HPCHCV077	A48711
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                                                                                                                                                                                                        Maertens G., Stuyver L.;
"NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE
AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS";
Patent number WO9613590-A/1, 09-MAY-1996.
INNOGENETICS NV (BE).
                                                                                                                                                                                                                                                                                                                                                                         Sequence 327 BP; 56 A; 102 C; 104 G; 51 T; 14 other;
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DEFINITION Hepatitis C virus côte gene, HN3 isolate.
                                                                          07-WAR-1997 (Rel. 51, Crested)
07-WAR-1997 (Rel. 51, Last updated, Version 1)
Sequence 1 from Patent W09613590.
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Local Similarity 100.0%;
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N-10 Submitted (22-NOV-1993) to the EMBL/GenBank/DDBJ databases. D. Qu, INSERM Unite 271, U. de Recherche sur les Hepatites,, le Sida et les Retrovirus Humains, 151 cours Albert Thomas, F 69424 Lyon Cedex Hepatitis C virus Viruses; ssRNA_positive-strand viruses, no DNA stage; Flaviviridae; Repatitis_C=like viruses. ö /note="region corresponding to the core protein of the polyprotein of $\ensuremath{\mathsf{HCV}}\xspace^{-1}$ ggccccaggttgggtgtgcgcgcgactaggaagacttccgagcggtcgcaacctcgtggc 208 aggogacagoctatococaaggotogtoggocogagggoaggtootgggotoagocoggg 268 181 AGCCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCAGGTCCTGGGCTCAGCCCGGG 240 269 taccettggccetetatggcaacgagggetgegggtgggcagggtggeteetgteece 328 88 9 Gaps Qu,D., Hantz,O., Gouy,M., Vitvitski,L., Li,J.S., Berby,F., Tong,S.P. and Trepo,C.
Theterogeneity of hepatitis C virus genotypes in France J. Gen. Virol. 75 (Pt 5), 1063-1070 (1994) 29 atgagcacyaatcctaaacctcaaaggaaaaccaaaacgtaacatcaaccgccgccacag ; Length 506; Indels VRL protein 4; Mismatches 23; Score 291; DB 117; Pred. No. 4.45e-221;

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/translation="mastropedgreterrepter developedgretergereder developedgreter developedgretergereder developedgreterg
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Bukh, J., Purcell, R.H. and Miller, R.H.
Sequence analysis of the 5' noncoding region of hepatitis C virus
Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 573)
Bukh, J., Purcell, R.H. and Miller, R.H.
At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative El gene of isolates collected worldwide Proc. Natl. Acad. Sci. U.S.A. 90 (17), 8234-8238 (1993)
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                                    Proc. Natl. Acad. Sci. U.S.A. 91, 8239-8243 (1994)
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5 RESULT

E05083 577 bp RNA PAT 26-N0V-1996 DNA encoding a part of antigen of type non-A non-B hepatitis virus. JP 1993176774-A/20 unidentified. q2173277 E05083 DEFINITION **ACCESSION** KEYWORDS SOURCE

unidentified unclassified. ORGANISM

Kunitada, S., Muneo, T., Rieko, F., Kaoru, S., Masako, C., Hajime, H., Naofumi, H., Akimasa, O., Noriyoshi, M., Takashi, K., Takeshi, T., (bases 1 to 577) REFERENCE AUTHORS

Haruhide, K., Kazumasa, Y. and Ken, O. . HEDATIFIS NON-A-NON-B ANTIGEN FRAGMENT, ITS PRODUCTION AND REAGENT FOR HEDATIFIS NON-A-NON-B DIAGNOSIS USING THE SAME Patent: JP 1993176774-A 20 20-JUL-1993; SHIMOTOONO KUNITADA, GREEN CROSS CORP.THE OS type non-A non-B hepatitis virus PN JP 1993176774-A/20 PD 20-JUL-1993 JOURNAL TITLE

18-DEC-1990 JP 90P 412020 SHIMOTOONO KUNITADA, TSUJIKAWA MUNEO, FURUTA RIEKO, PI 18-DEC-1991 JP 1991354708 18-DEC-1990 JP 90P 4120 OS PN PP PR PR COMMENT

MIYANO NORIYOSHI, KOBPYASHI TAKASHI, TAKAHASHI CHUGENJI MASAKO, HORII HAJIME, HAYASUKE NAOFUMI, OMIZU KAORU,

AKIMASA, PI MIYANO NORIYOSHI, KGBPYASHI TAKASHI, TAKAHASHI TAKESHI, PI KAMABE HARLHIDE,
PI YOKOYAMA KAZUMASA, OKABAYASHI KEN
PC C12N15/51, C07K13/00, C12P21/02, G01N33/53, G01N33/569, G01N33/576, (C12P21/02,

112 /organism="unidentified" Location/Qualifiers 179 g strandedness: Double; topology: Linear; hypothetical: No; anti-sense: No; 183 c 1..577 C12R1:19); æ 103 288888 source BASE COUNT FEATURES ORIGIN

Gaps ; 0 Length 577; Indels 4; Mismatches 26; Score 285; DB 69; Pred. No. 7.81e-216; Query Match 89.9%; Best Local Similarity 90.8%; 297; Conservative Matches

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181 AGGCGACAGCCTATCCCCAAGGCTCGYCGGAGGGCAGGTCCTGGGCTCAGCCCGGG 240 279 taccettggcccetetatggcaacgagggetgcggatggcgggatggetcctgtcaccc 338 δ 염

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339 egeggeteceggectagttggggeece 365 음

301 cccccrcrcccccATTcccccc 327 ð

no DNA stage; Flaviviridae, mainland of 28-SEP-1992 Hepatitis C virus (individual isolate China, strain HeBei) (library: NC1-18) cDNA to genomic RNA. isolated from Liu, C.-B VRL HPCCGENOM 9400 bp ss-RNA Hepatitis C China virus complete genome. L02836 Viruses; ssRNA positive-strand viruses, Hepatitis C-like viruses. and D Bi, S.-l., Bai, X.-H., Margolis, H.S. Complete hepatitis C virus genome complete genome; viral genome. (bases 1 to 9400) Hepatitis C virus q329739 9 DEFINITION ORGANISM ACCESSION REFERENCE AUTHORS KEYWORDS TITLE SOURCE RESULT LOCUS

C virus /organism="Hepatitis /isolate="China" /tissue lib="NC1-18" Location/Qualifiers /strain="HeBei" 1..9400 source mRNA COUNT FEATURES

Unpublished (1992)

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113, Japan (E-mail:PXN04522@niftyserve.or.jp, Tel:03-3813-6111 (ex.3224), Fax:03-3818-7177) /organism="Hepatitis C virus" Location/Qualifiers source FEATURES

/note="IFN-sensitive HCV from patient 1" /strain="HCV-1b"

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GLSAFSLHSYSPGEINRVASCLRKLGVPPLRTWRHRARSVRAKLLSQGGRAATCGRYL

Department of Internal Medicine; 1-5-45 Yushima, Bunkyo-ku, Tokyo

Nobuyuki Enomoto, Tokyo Medical and Dental University, Second

Submitted (08-MAY-1995) to the DDBJ/EMBL/GenBank databases.

Direct Submission

Enomoto, N.

Feb 23 20:47

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HPCKIR1 9410 bp ss-RNA VRL 02-FEB-1997
Hepatitis C virus (strain HCV-lb, clone HCV-K1-R1), complete genome
FNWAVKTKIKLTPIPAASQLDLSNWFVAGYSGGDVYHSLSRARPRWFMLCLLLLSVGV
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Pred. No. 7.81e-216;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C-like viruses GVRATRKTSERSQPRGRRQPIPKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRG VGDLCGSVFLVSQLFTFSPRRYETVQDCNCSIYPGHVSGHRWAWDMMMASPTTALVV SQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIVMLLFAGVDGNTYTTGARQ GRTVSRLTSIFTPGASQNIQLINTNGSWHINRTAINCNDSLQTGFIAALFYARRFNSS PALSTGLIHLHQNIVDVQYLYGVGSAVVSFAIKWEYVLLLFLLLADARVCACLWMMLL SRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLED GVNYATGNIPGCSFSIFLLALLSCLTIPASAYEVCNASGLYHVTNDCSNSSIVYEAQD GCPQRLASCRSIDKFAQGWGPITYAEGHDSDQRPYCWHYAPRPCGIVPAQQVCGPVYC FTPSPVVVGTTDRFGAPTYNMGANETDVLLLANTRPPQGNWFGCTWMNGTGFTKTCGG PPCNIGGAGNNTLTCPTDCFRKHPEATYAKCGSGPWLTPRCIVDYPYRLWHYPCTVNF VAQAEAALENLVVLNAASLAGVHGILSFLVFFCAAWYIKGKLVPGAAYALYGVWPLLL /translation="MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRI MIMHTPGCVPCVRENNSSRCWVALTPTLAARNASIPTTIRRHVDLLVGAAAFCSAMY SIFKVRMYVGGVEHRLTAACNWTRGERCDLEDRDRSELSPLLLSTTEWQILPCSFTTI Mobuyuki Enomoto, Tokyo Medical and Dental University, Second Department of Internal Medicine; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (E-mail:PXN04522@niftyserve.or.jp, Tel:03-3813-6111(ex.3224), Fax:03-3818-7177) IFN-resistant; ISDR; interferon sensitivity determining region; Yanamoto, C., Izumi, N., Marumo, F. and Sato, C. Comparison of full-length sequences of interferon-sensitive a resistant hepatitis C virus 1b. Sensitivity to interferon is Enomoto, N., Sakuma, I., Asahina, Y., Kurosaki, M., Murakami, T., Submitted (08-MAY-1995) to the DDBJ/EMBL/GenBank databases interferon-sensitive; interferon-resistant; IFN-sensitive; conferred by amino acid substitutions in the NS5A region HVR; hypervariable region. Hepatitis C virus (strain:HCV-1b) cDNA to genomic RNA, /note="IFN-resistant HCV from patient 1" Clin. Invest. 96 (1), 224-230 (1995) /organism="Hepatitis C virus" /product="polyprotein" /db_xref="PID:d1009706" /db_xref="PID:g1814085" /clone="HCV-K1-R1" /strain="HCV-1b" /codon_start=1 (bases 1 to 9410) (bases 1 to 9410) Unpublished (1995) 330..9362 Hepatitis C virus Direct Submission clone: HCV-K1-R1. 1..9410 (sites) Enomoto, N. Enomoto, N. 95340824 source ORGANISM TITLE JOURNAL AUTHORS MEDLINE AUTHORS JOURNAL REFERENCE AUTHORS REFERENCE JOURNAL REFERENCE CDS TITLE FEATURES

LQVWIPPLNVRGGRDAIILLTCAVHPELIFDITKIVLAILGPLMVLQAGIAKVPDFVR aogvirecilvrkvgggqyvqmafmklaeikgtsvydhltplrdwahtglrdlavave

PVVFSDMEIKIITWGGDTAACGDIIMGLPVSARRGREILLGPADSLEGOGWRLLAPIT **AYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSK** TLAGPKGP1TQMYTNVDQDLVGWPAPPCARSLTPCTCGGSDLYLVTRHADV1PVRRRG **MRSPVFTDNSSPPAVPQTFQVAHLHAPTGSGKSTKVPAAYAAQGYKVLVLMPSVTATL** GFGAYMSKAHGVDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIMCDECHS

DSRGSLLSPRPISYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETT

IDSTSILGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGK AIPIETIKGGRHLIFCHSKKKCDELAAKLSGLGLAAVAYYRGLDVSVIPASGDVVVVA

TDALMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRC

polyprotein; core protein; E1; E2; NS2; NS3; NS4A; NS4B; NS5A; NS5B; envelope protein; non-structural protein;

sequence. g1030706

D50480

ACCESSION KEYWORDS

LLLALPPRAYAMDREMAASCGGAVFIGLALLTLSPYYKVFLAKLIWWLQYLITRAEAQ

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δy	121	GCCCCCAGGNNGGGTGTGCGCGCGCGATCAGGAACATTCCGAGCGGTCACACATCGTGGC 180
qq	510	aggogacaactatcccaaaggctcgccgaggcccgagggcagggcctgggctcagccggg 569
δ	181	AGGGGACAGCCTATCCCCAAGGCTCGYCCGAGGGCAGGTCCTGGGCTCAGCCCGGG 240
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δ	241	TATCCTTGGCCCCTCTATGGCAATGAGGCCTGCGGGTGGGCGGGNTGGCTCCTGTCCCCC 300
qq	630	cgcggctcccggcctagttggggccc 656
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Æ	RESULT	
Š E	LOCUS DEFINITION	HPCNSISPC 1613 bp ss-RNA VRL 03-DEC-1992 Hepatitis C virus core protein (NSI) qene.
AC	ACCESSION	M74806
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SOI	SOURCE	Hepatitis C virus (individual isolate SP1) c
-	OKGANISM	n hepatitis C Vitus Viruses; ssNNA positive-strand viruses, no DNA stage; Flaviviridae;
B.	REFERENCE	,
7	AUTHORS	-
-	TITLE	At least five related, but distinct, hepatitis C viral genotypes
	JOURNAL	EXIST. Outl. Acad. Sci. U.S.A. 89, 7144-7148 (1992)
131	MEDLINE FEATURES	9233//88 Location/Qualifiers
	sonre	ce 11613 /organism="Hepatitis C virus"
BA. OR	BASE COUNT ORIGIN	/isolate=' 290 a 501 c
J	Query Ma	89.6%; Score 284; DB 122
	Best Local Si Matches 296	cal Similarity 90.8%; Pred. No. 5.846-215; 296; Conservative 4; Mismatches 26; Indels 0; Gaps 0;
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δ	1	ATGAGGAGGATCCTAAACCTGAAAGAAAACGAAAGGTAAGAGCGAACGGGGGCGCGCAA 60
qq	304	gacgicaagticccgggcggtggtcagatcgttggtggagtitacctgttgccgcgcagg 363
δò	61	GESCINNINNINNINCGGGTGGCGGTCAGATCGTTGGAGTTAACCTGTTGCCGCGCAGG 120
ąg	364	ggcccaggttgggtgtgcgcgcgactaggaagacttccgagcggtcgcaacctcgtgga 423
Q,	121	GCCCCAGCNNGGGTGTGCGCGCGCGACTAGGAAGACTTCCGAGCGGTCACACATCGTGGC 180
qa	424	aggogacaacctatccccaaggctcgccggcccgagggcagggcctgggctcagcccggg 483
Qy	181	AGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCAGGTCCTGGGCTCAGCCCGGG 240
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Patent number W09613590-A/5, 09-MAY-1996.
INNOGENETICS NV (BE).
Other publication AU 3844095 960523
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62 A; 105 C; 103 G; 54 T; 3 other;
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Sequence 5 from Patent W09613590.
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/translation="mSTNPKPQRKTKRNTNRRPQDVKFPGGGJUGGVYLLPRRGPRL AVRATRKTSERSQPRGRRQPIPKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRG van Doorn, L.J., Kleter, G.E., Stuyver, L., Maertens, G., Brouwer, J.T., Schalm, S.W., Heijtink, R.A. and Quint, W.G. Sequence analysis of hepatitis C virus genotypes 1 to 5 reveals multiple novel subtypes in the Benelux countries J. Gen. Virol. 76 (Pt 7), 1871-1876 (1995) ď ;**`** Doorn L.J., Diagnostic Centre SSDZ, Dept. of Molecular Biology, de Graafweg 7, PO Box 5010, 2600 GA, Delft, The Netherlands 2 (bases 1 to 346) Viridae; ss-RNA enveloped viruses; Positive strand RNA viruses; 121 ggccccaggttggctgtgcgcgcgactaggaagacttccgagcggtcgcaacctcgtgga 180 240 61 gacgttaagttcccgggcggtggtcagatcgttggtggagtttacctgttgccgcgcagg 120 181 AGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCAGGTCCTGGGCTCAGCCCGGG 240 241 taccettggcccetctatggcaatgagggettggggtgggcaggatggetectgtcaccc 300 1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCCCCCAK 60 Gaps Submitted (12-JAN-1994) to the EMBL/GenBank/DDBJ databases. 1 atgagcacgaatectaaacctcaaagaaaaccaaacgtaacaccaaccgccccacag ; 0 Length 346; Indels Score 283; DB 117; Pred. No. 4.36e-214; 4; Mismatches 27; /note="core region; pid:g443863" /codon start=1 /db_xref="PID:g443863" organism="Hepatitis C virus" 26 301 cgcggctctcggcctagctggggcccc 327 CGCGCTCTCGGCCCAATTGGGCCCC 327 111 g Location/Qualifiers SRPSWGPTDPRRR 89.3%; 90.5%; (bases 1 to 346) 296; Conservative Hepatitis C virus Hepatitis C virus Direct Submission 1..346 van Doorn, L.J. Togaviridae. Best Local Similarity 97201609 19 Query Match source ORGANISM BASE COUNT Matches JOURNAL MEDLINE 301 REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL KEYWORDS CDS TITLE FEATURES SOURCE ORIGIN

HCU10209 573 bp RNA VRL Hepatitis C virus isolate S45 core protein gene. U10209

Hepatitis C virus. Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

SOURCE ORGANISM

KEYWORDS

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SOURCE	CE	structural protein. Hepatitis C virus (isolate:HC-J2) cDNA to genomic RNA.
OR	ORGANISM	Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFEI	RENCE	Hepatitis C-like viruses. 1 (sites)
AU	AUTHORS	جہ ہے
II	TITLE	rukuda,2., isuda,f. and mismiru,3. Full-length sequence of a hepatitis C virus genome having poor homology to reported isolates, comparative study of four distinct
		include acted to the contract
JOU	JOURNAL MEDITNE	Virology 188 (1), 331-341 (1992) 92230232
REFE	REFERENCE	2 (bases 1 to 1863)
JOL	AUTHORS	
COMMENT	ENT	Data kindly submitted in computer readable form by: Hiroaki Okamoto
		Immunology Division Jichi Medical School
		Kawachi-gun Tochigi 320-04
		Phone: 0285-44-2111 x3334 Fax: 0285-44-1557.
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		LIMHAPGCVPCVRENNSSRCWVALTPTLAARNTSIPTTIRRHVDLLVGAATFCSAMY

406 t 539 g 574 c 344 BASE COUNT

ORIGIN

ö Gaps ; 0 Length 1863; Indels 4; Mismatches 27; Pred. No. 4.36e-214; Score 283; DB 122; ch 89.3%; 1 Similarity 90.5%; 296; Conservative Best Local Similarity Query Match Matches

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HPCKIR2 9410 bp ss-RNA VRL 02-FEB-1997 Hepatitis C virus (strain HCV-lb, clone HCV-K1-R2), complete genome IFN-resistant; ISDR; interferon sensitivity determining region; polyprotein; core protein; E1; E2; NS2; NS3; NS4A; NS4B; NS5A; interferon-sensitive; interferon-resistant; IFN-sensitive; NS5B; envelope protein; non-structural protein; sequence. g1030705 14 DEFINITION ACCESSION KEYWORDS

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus (strain: HCV-1b) cDNA to genomic RNA, Hepatitis C-like viruses. Hepatitis C virus clone: HCV-K1-R2. ORGANISM

HVR; hypervariable region.

SOURCE

Comparison of full-length sequences of interferon-sensitive and resistant hepatitis C virus 1b. Sensitivity to interferon is Enomoto, N., Sakuma, I., Asahina, Y., Kurosaki, M., Murakami, T., Yamamoto, C., Izumi, N., Marumo, F. and Sato, C. conferred by amino acid substitutions in the NS5A region AUTHORS TITLE

(sites)

REFERENCE

J. Clin. Invest. 96 (1), 224-230 (1995) (bases 1 to 9410) 95340824 JOURNAL MEDLINE REFERENCE

Unpublished (1995) Enomoto, N. JOURNAL AUTHORS

RSVWKDLQEDTETP I DTT I MAKNEVFCVQPEKGGRKP ARLI VFPD LGVRVCEKMALYD

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(bases 1 to 9410) Enomoto, N AUTHORS JOURNAL REFERENCE TITLE

Department of Internal Medicine; 1-5-45 Yushima, Bunkyo-ku, Tokyo Direct Submission Submitted (08-MAY-1995) to the DDBJ/EMBL/GenBank databases. Nobuyuki Enomoto, Tokyo Medical and Dental University, Second 113, Japan (E-mail:PXN04522@niftyserve.or.jp, Tel:03-3813-6111(ex.3224), Fax:03-3818-717)

Location/Qualifiers

/note="IFN-resistant HCV from patient /organism="Hepatitis C virus" 1..9410

source

FEATURES

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2757..3407
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Best Local Similarity 90.5%;
Matches 296; Conservative
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VRL

9410 bp ss-RNA

HPCK1S2

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RESULT LOCUS

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MIMHTPGCVPCVPEANSSRCMVALTPTIAARNSSVPTTTIRRHVDLLVGAAAFCSAMY
VGDLCGSVFLVSQLFTFSPRRHETVQDONGSTYPGHVSGHRAAMDMMMSPTTALVV
SQLIR.IPQAVMDMYAGAHMGVLAGLAYYSMVGNWAKVLIVMLLFAGVDGRTVVTGGAQ
RTTQRILASLFTFGQQRIQLYNTNGSWHINTFALMCNDSLMTGFLAALFYTHRFNS
GCPPRIASCRSIDAFAQGMGPITYAEOGSSDQRPYCGHYARPROG CIVPASEVGCPYYG
FTPSPVVVGTTDRSGAPTYSWGENETDVLLIANNTRAPQGNWFGCTWMNGTGFTKTCGG SRP SWGP TDPRRRSRNLGKV I DTLTCGFAD LMGY I PLYGAP LGGA SRALAHGVRV LED GVNYATGNLPGCSFSIFLLALLSCLTIPASAYEVRNASGVYHVTNDCSNASIVYEAAD LQVWIPPLNVRGGRDAIILLTCALHPELIFSITKILVAILGPLMVLQAGITKMPYFVR AQCLIRACMIVRKVAGGHYVQMAFWKLAALTGTYVYDHLTPLQDWAHAGLRDIAVAVE PVVFSDMETKI ITWGADTAACGDIILGLAVSARRGKEIFLGPADSLEGSGWRLLAPIT AYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCTNGVCWTVYHGAGSK Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GVRATRKTSERSQPRGRRQPIPKARQPEGRAWAQPGYPWPLYGNEGMGWAGWLLSPRG PPCNIGGVGNNTLICPIDGFRKHPEATYTKCGSGPWLTPRCMVDYPYRLMHYPCTVNF TIFKVRMYVGGVEHRLNAACNWTRGERCDLEDRDRSELSPLLLSTTEWQILPCSFTTL PVLSTGLIHLHQNIVDVQYLYGVGSAVVSFVIKWEYILLLFLLLADARVCACLWMMLL I AQAEAALENI.VVI.NAASVAGAHGFI.SFI.VFFCAAWY IKGKI.VPGAAYAFYGVWPI.LL LLLALPPRAYAMDREMAASCGGAVFVGLALLTLSPHYKVVLARLIWMLQYFITRAEAC TLAGSKGP ITQMYTNVDQDLVGWQAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRG Hepatitis C virus (strain HCV-1b, clone HCV-K1-S2), complete genome /translation="MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRI Department of Internal Medicine; 1-5-45 Yushima, Bunkyo-ku, Tokyo Yamamoto, C., Izumi, N., Marumo, F. and Sato, C. Comparison of full-length sequences of interferon-sensitive and interferon-sensitive; interferon-resistant; IFN-sensitive; IFN-resistant; ISDR; interferon sensitivity determining region; polyprotein; core protein; E1; E2; NS2; NS3; NS4A; NS4B; NS5A; Submitted (08-MAY-1995) to the DDBJ/EMBL/GenBank databases. Nobuyuki Enomoto, Tokyo Medical and Dental University, Second resistant hepatitis C virus 1b. Sensitivity to interferon is Enomoto, N., Sakuma, I., Asahina, Y., Kurosaki, M., Murakami, T., conferred by amino acid substitutions in the NS5A region Hepatitis C virus (strain: HCV-1b) cDNA to genomic RNA /note="IFN-sensitive HCV from patient 2" NS5B; envelope protein; non-structural protein; 113, Japan (E-mail:PXN04522@niftyserve.or.jp, Tel:03-3813-6111 (ex.3224), Fax:03-3818-7177) J. Clin. Invest. 96 (1), 224-230 (1995) /organism="Hepatitis C virus" /product="polyprotein" /db_xref="PID:d1009711" /db_xref="PID:g1814089" Location/Qualifiers /clone="HCV-K1-S2" HVR; hypervariable region. /strain="HCV-1b" Hepatitis C-like viruses. /codon_start=1 (bases 1 to 9410) (bases 1 to 9410) Unpublished (1995) Hepatitis C virus Direct Submission clone: JCV-K1-S2. 1..9410 Enomoto, N. (sites) Enomoto, N. sednence. 95340824 q1030704 Source DEFINITION REFERENCE AUTHORS TITLE JOURNAL ORGANISM ACCESSION NID KEYWORDS JOURNAL REFERENCE AUTHORS JOURNAL MEDLINE REFERENCE AUTHORS CDS TITLE FEATURES SCURCE

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TDS TS I LGI GTVLDQAETAGARLVVLATATPPGS VTVPHPN I EEVALSNI GEI PFYGK AIP I ET IKGGRHLIFCHSKKKCDELAAKLSGLGI NAVAYYRGLDVSVI PASGDVVVVA FDA LMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRG RAGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVWQ LIR LIKPTLHGPTP LLYR LGAVQNEVILTHP ITKY IMACMSADLEVVTSTWV LVGGVLA ALAAYCLTTGSVVIVGRIILSGKPAIIPDREVLYREFDEMEECASHLPYIEQGMQLAE QFKQKALGLLQTATKQAEAAAPVVESKWQALETFWAKHMWNFISGIQYLAGLSTLPGN

JHLEFWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKC

GFGAYMSKAHGVDPNIRTGVRTITTGAPITYSTY GKFLADGGCSGGAYDIIICDECHS

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510 aggcgacaacctatccccaaggctcgccagcccgagggcagggcctgggctcagcccggg 569

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929 cgcggctctcggcctagttggggcccc 630

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RLHQWINEDCSTPCSGSWLRDVWDWICTVLTDFKTWLQSRVLPRLPGVPFLSCQRCYK GVWRGDGIMQTTCPCGAQITGHVKNGSMRIVGPKTCSNTWHCTFP INAYTTGPCTPSP APNYSRALWRVAAEEYVEVTRVGDFHYVTGMTTDNIKCPCQVPAPEFFKELDCVRLHR YAPASKPLLRDEVTFQVGLAQYVVGSQLPCEPEDVAVLTSMLTDPSHITAEAAKRRL

ARGSPPSLASSSASQLSAPSLKATCTTRHDSPDADLIEANLLWRQEMGGNITRVESEN

KVVI LDSFEP LRAEEDEREVS LPAEI LRKSRKFP PAMP IWARPDYNPP LIESWKDPD) VPPVVHGCPLPPTKAPPIPPPRRKRTVVLTESTVSSALAELATKTFGSSESSAADSG1

GLGKVLVDILAGYGAGVAGALVAFKVMSGDMPSTEDLVNLLPAILSPGALVVGVVCAA : LRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTQILSSLTITQLLK

PAIASLMAFTASITSPLTTQHTLLFNILGGWVAAQLAPPRAASAFVGAGIAGAAVGSI

ATAPPDQPSNDGDAGSDVESYSSMPP.LEGEPGDPDLSDGSWSTVSEEAGEDVVCCSMS /TWTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSASQRQKKVTFDRLQVLD RSVWKDLLEDTETPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYD EES I YQCCDLAPEARQA I RSLTERLY I GGPLTNSKGQNCGYRRCRASGVLTTSCGNTL

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301 ceceectereecceAntreecece 327

Search completed: Mon Feb 23 20:50:29 1998 Job time : 446 secs.



TCYLKATAACRAAKLÕDCTMLVCGDDLVVI CESAGTQEDAASLRVFTEAMTRYSAPPG DPPQPEYDLELLITSCSSNVSVAHDASGKRVYYLTRDPTTP LARAAWETARHTPVNSWL GNI IMYAPTLMARMI LMTHFFS I ILLAQEQLEKALDCQIYGACYS I EP LDLPQI I QRLH

VVSTLPQAVMGPSYGFQYSPGQRVEFLVNAWKSKKCPMGFAYDTRCFDSTVTESDIRV

DHYRDVLKEMKAKASTVKARLLSVEEACKLTPPHSARSKFGYGAKDVRNLSSRAINH:

GLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRAKLLSQGGRAAICGKYL

FINMAVRTKLKLTPIPAASQLDLSGWFVAGYSGGDIYHSVSRARPRWFMWCLLLLSVGV

/product="core protein" 903..1478

GIYLLPNR' 330..902

> mat_peptide mat_peptide

product="E1"

1479..2756

mat_peptide

'note="hypervariable region (HVR)"

..3407 3408..5300 1..5462 5463..6245 246..7586 6954..7073

/product="E2" 1479..1559

misc_feature mat_peptide

WAR IN

ö Indels 0; Gaps Score 283; DB 122; Length 9410; Pred. No. 4.36e-214; 4; Mismatches 27; Query Match 89.3%; Best Local Similarity 90.5%; Matches 296; Conservative

330 atgagcacgaatcctaaacctcaaagaaaaaccaaacgtaacaccaacgccgcccacag 389

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/note="interferon sensitivity determinig region (ISDR)" 7587..9359

product="NS5A"

misc_feature

mat_peptide

'product="NS4A" product="NS4B"

'product="NS3" product="NS2"

mat_peptide

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mat_peptide mat_peptide mat_peptide 1983 t

2715 g

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BASE COUNT ORIGIN

/product="NS5B"

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 56.27 Seconds 670.654 Million cell updatas/sec Mon Feb 23 20:50:49 1998; Run on:

Tabular output not generated.

>US-08-836-075A-1

(1-327) from USO8836075A.seq 317 Description:

Perfect Score:

1 ATGAGCACGATCCTAAACC.......CTCGGCCCAATTG.GCCCC 327
TACTCGTGCTTAGGATTTGG........GAGCCGGGTTAACGGGGG N.A. Sequence:

TABLE default Scoring table:

Dbase 0; Query 0 Gap 6 STD Mmatch

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159651 seqs, 57698962 bases x 2 Searched:

Post-processing: Minimum Match 0%

Listing first 45 summaries

n-geneseq30 Database:

| ipart| 2:part2 3:part3 4:part4 5:part5 6:part2 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part12 15:part12 15:part13 16:part16 17:part17 16:part18 20:part20 2:part21 22:part23 23:part23 23:part23 23:part23 23:part23 23:part24 25:part20 23:part20 23:part20 23:part20 23:part20 23:part20 23:part30 23:p

Mean 7.918; Variance 5.033; scale 1.573 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

red. No.	.34e-189	.16e-167	1.16e-167	.49e-166	.49e-166	.49e-166	
Δ,	dk	80	180	typ		iso 2	
Description	Hepatitis C virur	Hepatitis C v	Hepati	Her			
11	T27937	T16620	T16621	T27939	021747	T16617	
98	25	21	21	25	m	21	•
Query Match Length DB	327	573	573	327	570	573	
Query Match	100.0	89.9	89.9	89.3	89,3	89.3	
Score	317	285	282	283	283	283	
Result No.	1	7	٣	4	2	9	

Mome/fuller/feb.1098/US-08-836-075A-1.mg Feb 23 20:48

49e	.34e-16	.34e-1	5.34e-165	.34e-1	.34e-1		.34e-1	.34e-1	.34e-1	.34e-1	5.34e-165	.34e-1	.47e-1	7		-	_	_	[5e-1	_	5e-1	7	.15e-1	.30e-1	$\overline{}$.45e-1	5e-1	.45e-1	.45e-1	_	2.45e-162	.45e-1	.45e-1	2.45e-162	2.45e-162	2.45e-162	.45e-16	
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۲ 0	0 0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	58	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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T27937 standard; DNA; 327 BP. 07-MAR-1997 (first entry) T27937;

RESULT

Hepatitis C virus type 1d isolate BNL1 bases 1-310.

Hepatitis C virus; Subtype; polymerase chain reaction; amplification; PCR; primer; probe; antibody; infection; ss. Hepatitis C virus. WO9613590-A2.

09-MAY-1996. 23-67-1995, E04155. 21-687-1994, EP-870166. 28-JRN-1995, EP-870076. (INNO-) INNOGENETICS NV.

Maertens G, Stuyver L; WPI; 96-251460/25.

P-PSDB; R96526.

Hepathtis C virus poly;nucleic acid unique to unidentified sub:type - used to develop probes and primers for new sub:types and vaccines to prevent and treat infection Claim 6; Fig. 3; 150pp; English.

m

The new HCV types were isolated from patients with chronic HCV from the Benelux countries, France, Cameroon and Vietnam, because of their aberrant reactivities. The RNA was extracted, CDNA synthesised and PCR amplified, cloned and genotyped. The 5'UR, Core/EI and NSSB regions were sequenced either directly or partially and used to classify the new viruses into (subltypes based on comparison with known sequences. The sequences were used to generate the peptides R96424-R96524. The sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect hepatitis C virus subtypes different from subtypes la-c, 2a-d, 3a-f, 4a-j, 5a and 6a. They esp. from the novel subtypes Id-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-c or types 9, 10 or 1l. The sequences corresp. to the 5' untranslated region (UR), the Core/El, NS4 or NS5B regions of the genome. This sequence represents nucleotides 1-310 from the HCV type Id isolate sequences T27937-T27989 represent novel sequences isolated from anti-HCV antibodies, for HCV typing or to prevent HCV infections. Sequence 327 BP; 56 A; 102 C; 104 G; 51 T;

Gaps .; 0 Query Match 100.0%; Score 317; DB 25; Length 327; Best Local Similarity 100.0%; Pred. No. 5.34e-189; 0; Mismatches 0; Indels 327; Conservative Matches

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1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGAAACGAACCCAACCACCCCCCAK 60 1 atgagcacgaateetaaaeeteaaagaaaaeeaaaegtaaeaccaacegeegeeteak 60 ű ç ď

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121 ggccccaggnngggtgtgcgcgcgactaggaagacttccgagcggtcacaacctcgtggc 180 g

181 aggegaeagectatececaaggetegyeggyeegagggeaggteetgggeteageeeggg 240 Ş g

Ş g Ş

CGCGCTCTCGCCCCATTGGGCCCC 327 egeggeteteggeecaattggggeeee 327 301 301 g Ş

LT 2 T16620 standard; cDNA; 573 BP. 01-0CT-1996 (first entry) T16620;

Hepatitis C virus isolate P10 core protein gene. HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;

Location/Qualifiers Hepatitis C virus. hepatitis; ss. Key

/*tag= a

/note= "does not contain stop codon" /product= core protein

WO9605315-A2.

15-AUG-1995; U10398 22-FEB-1996,

(USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH.

15-AUG-1994; US-290665.

DNA and amino acid sequence of HCV envelope 1 and core proteins Bukh J, Miller RH, Purcell RH; WPI; 96-139709/14. P-PSDB; R92946.

used to determine HCV genotype and as vaccines against HCV infection claim 3; Page 156; 340pp; English.
T16610-T16661 are cDNAs encoding a core protein gene of 52 HCV isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may

179 6; used in the prevention of HCV infection. 185 C; 96 A; Sequence

113 T;

Gaps ; 0 Length 573; 4; Mismatches 26; Indels Score 285; DB 21; I Pred. No. 1.16e-167; 86.68 Best Local Similarity 90.8%; Matches 297; Conservative Query Match

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9 1 atgagcacjaatcctaaacctcaaagaaaaaccaaacgtaacaccaacugccgcccacag

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61 gacytcaagttcccgggcggtggtcagatcgttggtggagtttacctgttgccgcgcagg 120 셤

121 ggccccaggttgggtgtgcgcgcgactaggaagacttccgagcggtcgcaacctcgtgga 180

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240 aggogacaacctatccccaaggctcgccggcccgagggcagggcctgggctcagcccggg 181 염

240 õ

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301 cgtggctctcggcctagttggggcccc 327 q

301 cccccrccccccaltcccccc 327

δ

Hepatitis C virus isolate DK1 core HCV; E1; envelope 1; core protein; J 3 T16621 standard; cDNA; 573 T16621; 01-0CT-1996 (first entry) Hepatitis C virus. hepatitis; ss.

protein gene. HCV genotyping; antibody; vaccine;

Location/Qualifiers /product= core_protein /*tag= a

/note= "does not contain stop codon" WO9605315-A2. 22-FEB-1996.

15-AUG-1995; U10398.

15-AUG-1994; US-290665

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claim 6; Fig 3; 150pp; English.

The sequences 12/937-71989 represent novel sequences isolated from hepatitis C virus subtypes different from subtypes la-c, 2a-d, 3a-f, 4a-j, 5a and 6a. They esp. from the novel subtypes 1d-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-z or types 9, 10 or 11. The sequences corresp. to the 5 untranslated region (UR), the Core/El, NS4 or NS5B regions of the genome. This sequence represents nucleotides 1-310 from the HCV type 1d isolate BNL2. Benelux countries, France, Cameroon and Vietnam, because of their aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The 5'UR, Core/El and NS5B regions were sequenced either directly or partially and used to classify the new viruses into (sub)types based on comparison with known sequences. The new HCV types were isolated from patients with chronic HCV from the 61 gacgicaagnicocgggiggiggiggicagaicgitggiggiggagittaccigitgccgcagg 120241 catccctggcccctctatggcaatgagggctgcggatgggcgggatggctcctgtccccc 300 The sequences were used to generate the peptides R96424-R96524. The sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect 1 atgagcacgaatcctaaacctcaaagaaaaaccaaacgtaacaccaacgccgcccacag 60 Hepatilis C virus poly:nucleic acid unique to unidentified sub:type used to develop probes and primers for new sub:types and vaccines anti-HCV antibodies, for HCV typing or to prevent HCV infections. Sequence 327 BP; 62 A; 105 C; 103 G; 54 T; 4; Mismatches 27; Indels Score 283; DB 25; I Pred. No. 2.49e-166; 327 301 egeggeteteggeecagttggggeece 327 301 CCCGCTCTCGGCCCAATTGGGGCCCC to prevent and treat infection BP. 88.38; Best Local Similarity 90.5%; 296; Conservative entry) Q21747 standard; DNA; 570 10-AUG-1990; JS-566209. 22-JUN-1992 (first 12-AUG-1991; U05728, HCV clone Th cDNA. Hepatitis C virus. 20-FEB-1992. W09202642-A. HCV1; ss. Query Match 021747; Matches RESULT
1D 02
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PD 2 염 ద g 쇰 염 g à à à ð δ à ö aggogacaacctatccccaaggotcgrcggcccgaggycayggcctgggctcagcccggg 240 isolates. The isolated sequences are useful for the prodn. of primers ggccccaggttgggtgtgcgcgactaggaagacttccgagcggtcgcaacctcgtgga 180 gacgicaagiicccgggcggigitcagaicgiiggiggagiilaccigiigccgcgcagg 120 61 GGSGTNNNNNNCCGGGTGGCGGTCAGATCGTTGGTGCAGTTTACCTGTTGCCGCGCAGG 120 121 GCCCCCAGGNNGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGCGTCACAACCTCGTGGC 180 taccettggcccetetatggcaatgaggcatggggtgggcaggatggeteetgtcaece 300 Hepatitis C virus type 1d isolate BNL2 bases 1-310. Hepatitis C virus; subtype; polymerase chain reaction; amplification; used to determine HCV genotype and as vaccines against HCV infection Claim 3; Page 156-157; 340pp; English. 9 Gaps proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs 1 atgagcacgaatcctaaacctcaaagaaaaaccaaacgtaacaccaaccgccgccacag can be used in vaccines for immunising against HCV infection. The proteins T16610-T16661 are cDNAs encoding a core protein gene of 52 HCV ; 0 Score 285; DB 21; Length 573; 113 T; 4; Mismatches 26; Indels P-PSDB; R92947. DNA and amino acid sequence of HCV envelope 1 and core Pred. No. 1.16e-167; 177 G; PCR; primer; probe; antibody; infection; ss. used in the prevention of HCV infection. Sequence 573 BP_i 98 A_j 185 C_i (USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH. cgcggctctcggcctagttggggcccc 327 Bukh J, Miller RH, Purcell RH; WPI; 96-139709/14. JT 4 T27939 standard; DNA; 327 BP. 89.68 Best Local Similarity 90.8%; Matches 297; Conservative 10-MAR-1997 (first entry) 21-OCT-1994; EP-870166. 28-JUN-1995; EP-870076. (INNO-) INNOGENETICS NV Stuyver L; 23-OCT-1995; E04155 Hepatitis C virus. WO9613590-A2. WPI; 96-251460/25 09-MAY-1996. Maertens G,

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                                                                                                                                                Score 283; DB 3; Length 570;
Pred. No. 2.49e-166;
                                                                                                                                                                       4; Mismatches 27; Indels
                                                                                   Disclosure; Fig 2; 67pp; English.
The sequences represented in Q21746-50 are DNA consensus sequences for five different HCV isolates from different
(CHIR-) CHIRON CORP.
Houghton M, Choo QL, Kuo G, Weiner AJ, Urdea MS, Irvine
                                                                                                                              116
                                                                                                                             177 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus isolate S45 core protein gene.
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15-AUG-1994; US-290665.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                   geographic locations (Japan and U.S.).
                                                                                                                              183 C;
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T16617 standard; cDNA; 573 BP.
                                                                                                                              94 A;
                                                                                                                                                  Match 89.3%;
Local Similarity 90.5%;
Hes 296; Conservative
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                                                                                                                              570 BP;
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Hepatitis C virus.
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                      Kolberg JA;
                                                                                                                                Sequence
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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection claim 3; Page 154, 340pp, English.
T16610-T1661 are cabNa encoding a core protein gene of 52 HCV isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 gacgicaagitcccgggtggcggtcagatcgttggtggagtttacctgttgccgcgcagg 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 120 | 12
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                                                                                                                                                                                                                                                                                                             are also useful for HCV genotyping. Proteins encoded by the CDNAs
                                                                                                                                                                                                                                                                                                                                                                                can be used in vaccines for immunising against HCV infection. The
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Pred. No. 2.49e-166;
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HCV; detection; antigen; vaccine;recombinant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention of HCV infection. 573 BP; 95 A; 189 C;
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WPI, 93-130639/16.
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Best Local Similarity 90.5%;
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RNA was extracted from the plasma of Japanese patients whose HBs antigen was negative and with a GPT over 100. cDNA was synthesised from the RNA and cloned into lambda gtl1 and screened using HCV infected chimpanzee plasma to isolate HCV clones. The DNA sequence is useful in detection of HCV virus. The polypeptide it produces may be used as an antigen in the prepn. of HCV vaccine. Sequence 9391 BP; 1861 A; 2840 C; 2696 G; 1994 T; Query Match 89.3%; Score 283; DB 6; Length 9391; Best Local Similarity 90.5%; Pred. No. 2.49e-166; Matches 296; Conservative 4; Mismatches 27; Indels 0; Gaps 0;	305 atgagcacgaatcctaaacctcaaagaaaaccaaacgtaacaccaaccgccgcccacag	425 ggcccaggttgggtgtggscggtcagagacttccgagcgtcgcaacccqtgga 484	SOL	28-APR-1993; KR-007231. (LUCK-) LUCKY CO LTD. (Cho JM, Choi DS, Choi DY, Kim CH, Kim IS, So HS; Yang JJ.; WPL; 94-358478/44. P-PSDB; R62862. Kit for simultaneous diagnosis of hepatitis B and C - comprising From or more hepatitis B and C virus antigenic proteins including From or more epitope(s) Disclosure, Fig 1; 89pp; English. This sequence encodes the KHCV core 14 protein, a preferred antigen for use in an immunodiagnostic kit for simultaneous detection of
8888888	8 9 8 9 4	6 6 6 6 6	PP PF FF F	PR PI PI PT PT PT CC

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hepatitis C and B viruses. The kit comprises antigenic proteins from both viruses. The HCV protein is pref. one of KHCV CORE 14, KHCV 897, KHCV NS4E, KHCV NS4ELE2 or KHCV NS5-1.2 proteins; the HBV protein Pro SS SAg protein. Sequence 384 BP; 76 A; 120 C; 121 G; 67 T;
                                                                                                                                                             .
0
                                                                                                                    Length 384;
                                                                                                                   Query Match 88.6%; Score 281; DB 12; Length 38-Best Local Similarity 90.5%; Pred. No. 5.34e-165; Matches 296; Conservative 3; Mismatches 28; Indels
     88888
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240 181 AGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCCAGGTCCTGGGCTCAGCCCGGG 240 121 ggccccaggttggggtgtgcgcgcgactaggaagacttccgagcggtcgcaacctcgtgga 180 181 aggcgacagcctatccccaaggctcgccggcccgagggcagggcctgggctcagcccggg g g δ δ ð

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g ò

Fragment of hepatitis C virus J7 isolate C/E domain. Hepatitis C virus; HCV-J1; HCV-J7; vaccines; NANBH; ss. Hepatitis C virus. Location/Qualifiers H. 011075 standard; DNA; 552 30-MAY-1991 (first entry) /label= HCV-J1 C/E domain 91..552 EP-419182-A. /*tag= a 011075; Key RESULT 110 011 1

27-MAR-1991. 17-SEP-1990; 310149. 15-SEP-1989; US-408045. 21-DEC-1989; US-456142. (CHIR-) CHIRON CORP.

New isolates J1 and J7 of hepatitis C virus - contg. specified DNA and amino acid sequences, used in diagnosis, recombinant Miyamura T, Saito T, Houghton M, Weiner AJ, Han J; Kolberg JR, Chata T-A, Irvine BD; WPI; 91-088781/13. P-PSDB; R11274. protein prodn. and vaccine

Disclosure; fig 1: 109pp; English.
This is a fragment of the hepatitis C virus (HCV) J7 isolate C/E domain. This is one of the domains of the viral isolate exhibiting heterogeneity w.r.t the HCV1 isolate. This sequence has an important potential use as a probe in diagnostic assays and vaccine

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                                                                                                                                                 271 aggcgacaacctatccccaaggctcgccggcccgagggcaggacctgggctcagcctggg 330
                                                                                                                                                                                                                                                tatecttggecectetatggeaatgaggetwggggtgggeaggatggeteetgteacee 390
                                                                                                          91 atgagcacaaatcctaaaccysaaagaaaaaccaaacgtaacaccaaccgtcgcccacag 150
                                                                                                                    Gaps
development. Antibodies directed against it can be used for screening antiviral agents and for isolation of non-A, non-B hepatitis (NANBH).
                                                                                      ;
;
                                                                Score 281; DB 2; Length 552;
Pred. No. 5.34e-165;
11; Mismatches 28; Indels
                                              103 T;
                                              176 G;
                                              161 C;
                                                                                                                                                                                                                                                                                                                      98 A;
                                                                 Query Match 88.6%;
Best Local Similarity 88.1%;
Matches 288; Conservative
                                See also Q11076-79.
                                             552 BP;
                                                Sequence
                                                                                                                                                                                                                                                                               331
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T16610-T16661 are cDNAs encoding a core protein gene of 52 HCV isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs 01-007-1996 (first entry)
Hepatitis C virus isolate D1 core protein gene.
HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; used to determine HCV genotype and as vaccines against HCV infection DNA and amino acid sequence of HCV envelope 1 and core proteins 15-AUG-1995, U10398.
15-AUG-1994, US-290665.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
(USSH) US SEC DEPT HEALTH.
Bukh J, Miller RH, Purcell RH;
WPI; 96-139709/14.
P-PSDB; R92944. /note= "does not contain stop codon" Location/Qualifiers Claim 3; Page 155; 340pp; English. T 10 T16618 standard; cDNA; 573 BP. /product= core_protein Hepatitis C virus. WO9605315-A2. 22-FEB-1996. hepatitis; /*tag= a T16618;

Hepatitis C virus isolate 110 core protein gene. HCV; El; envelope 1; core protein; HCV genotyping; antibody; vaccine;

T16622 standard; cDNA; 573 BP 01-0CT-1996 (first entry) Location/Qualifiers

Hepatitis C virus. hepatitis; ss.

Key

1..573

T16610-T16661 are cDNAs encoding a core protein gene of 52 HCV isolates. The isolated sequences are useful for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs

used to determine HCV genotype and as vaccines against HCV infection DNA and amino acid sequence of HCV envelope 1 and core proteins -

Claim 3; Page 157; 340pp; English.

Bukh J, Miller RH, Purcell RH; WPI; 96-139709/14. P-PSDB; R92948.

22-FEB-1996. 15-AUG-1995; U10398. 15-AUG-1994; US-290665. (USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH.

/note= "does not contain stop codon"

WO9605315-A2.

/product= core_protein

/*tag= a

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ö 240 181 AGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGCCAGGTCCTGGGCTCAGCCCGGG 240 saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection.
Sequence 573 BP; 100 A; 184 C; 174 G; 115 T; 01-OCT-1996 (first entry)
Hepatitis C virus isolate US6 core protein gene.
HCV; El; envelope 1; core protein; HCV genotyping; antibody; vaccine; 9 Gaps can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, 181 aggcgacaacctatccccaaggctcgccggcccgagggtagggcctgggctcagcccggg 1 atgagcacgaatcctaaacctcaaagaaaaaccaaacgtaacaccaaccgcccacag ö Length 573; 4; Mismatches 28; Indels Score 281; DB 21; I Pred. No. 5.34e-165; (USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH. 301 cgcggttctcggcctagttggggcccc 327 JIIII IIIIIIII I IIIIIIIII 301 CGCGCTCICGCCCCAATTGGGGCCCC 327 /product= core_protein /note= "does not contain stop codon" Location/Qualifiers T 13 T16619 standard; cDNA; 573 BP Query Match 88.6%; Best Local Similarity 90.2%; Matches 295; Conservative 22-FEB-1996. 15-AUG-1995; U10398. 15-AUG-1994; US-290665. 1..573 Hepatitis C virus. hepatitis; ss. W09605315-A2. T16619; 888888

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CC can be used in vaccin	can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum.	ខខ	can be used in vaccines for immunisir proteins may also be used to detect
saliva, lymphocy used in the prev Sequence 573 B	saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection. Sequence 573 BP; 96 A; 184 C; 177 G; 116 T;	သည် လ	saliva, lymphocytes or other mononucused in the prevention of HCV infect. Sequence 573 BP; 97 A; 185 C,
Query Match 88.6%	88.6%; Score 281; DB 21; Length 573;	Õ M X	Query Match 88.6%; Score 28:
Best Local Similarity 90.2%	90.2%; Pred. No. 5.34e-165;		Best Local Similarity 90.2%; Pred. No.
Matches 295; Conservative	vative 4; Mismatches 28; Indels 0; Gaps 0;		Matches 295; Conservative 4; Misr
Db	atgagcacgaatcctaaacctcaaagaaaaccaaacgtaacaccaaccgccgccacag 60	Db	1 atgagcacgaatcctaaacctcaaagaaaaa
		Qy	
Db 61 gacgtcaagttcccg : (y 61 GGSCTNNNNNNCCC	gacgtcaagttcccgggcggtggtcagatcgttggtggagtttacctgttgccgcgcagg 120 :	Db Qy	61 gacgtcaagttcccgggcggtggccagatcgl :
Db 121 ggcccaggttgggt	ggcccaggttgggtgtgggcgcgactaggaagacttccgagcggtcgcaacctcgtgga 180	Ob	121 ggcccaggttgggtgtgcgcgcgctagar
		Oy	
Db 181 aggcgacaacctatcon	tat ccccaagget cgccggcccgaggtagggctggget cagcccggg 240	Db	181 aggcgacaactatcccaaggctcgccggcc
		Qy	
Db 241 taccttggccctc	taccttggcccttatggcaacgaggcttggggtgggcaggatggtcctgtcacc 300	DP	241 caccttggcccttatggcaatgagggtt
		Qy	
Db 301 cgcggctcccggcct:	<pre>gcctagttggggccc 327 iii i GCCAATGGGGCCC 327</pre>	Db	301 cgcggctctcggcctagttggggcccc 327
		Qy	
ACSULT 14 TI 6625 standard; CDNA; 573 BP. AC 716625, DT 01-OCT-1996 (first entry) DE Hepatitis C virus isolate IND8 corr M HCV; El; envelope 1; core protein; KW HCV; El; envelope 1; core protein; FY C DE 1573 FT / tag= a FT / product= core_protein FT / product= core_protein FT / product= core_protein FT / product= core_protein FT / product= 220665. PR 15-AUC-1995; U10398. PR 15-AUC-1995; U10398. PR 15-AUC-1995; U10398. PR 15-AUC-1995. PR 15-AUC-1995; U10398. PR 15-AUC-19951. PR 18-AUC-19951. PR 18-AUC-19951. PR 18-AUC-19965. PR 18-AUC-19966. PR 18-AUC-19966.	17 14 17 16625 standard; CDNA; 573 BP. 17 16625 17 16625 17 16625 17 16625 18 16 16 16 16 16 16 16 16 16 16 16 16 16	RESULT 10 04 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1.T 15 0.44921 standard; DNA; 686 BP. 0.44921; 0.4-0CT-:994 (first entry) Hepatitis C virus; FCV; non-A, non-B antisense oligonucleotide; translatis 5'-untranslated region; 5'-UTR; hybr: Hepatitis C virus. 1.341 /*tag= a 342686 /*tag= a 342686 /*tag= b product= Core protein //tag= b protein //tag= core protein /

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immunising against HCV infection. The otetect antibodies against HCV in serum, mononuclear cells. The antibodies may be
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        ni haan ad nea
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177 G; tion.

114 T;

81; DB 21; Length 573; o. 5.34e-165; smatches 28; Indels 0; Gaps

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9 9 accaaacgtaacaccaaccgccgccacag

gttggtggagtttacctgttgccgcgcagg 120 GITGETGAGTTTACCTGTTGCCGCGCAGG 120 240

egion and part of core region.
B hepatitis virus; NANBHV;
ion inhibition; therapy;
oridisation target; ss.

INST.

RESULT 11D 711 1D 711 1

olementary to hepatitis C viral replication, to treat related Hanecak RC; Hamada F, Har T, Nozaki C;

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        Disclosure; Fig 1; 91pp; English.
Oligonucleotides which are complementary to part of the hepatitis C virus genomic or messenger RNA are claimed. Preferred antisense oligonucleotides are complementary to RNA comprising regions of the 5'-UTR, esp. the 5'end hairpin loop, 5'end 6bp repeat and 5'end untranslated region.
                                                                                                                  Gaps
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                                                                                           Query Match 88.6%; Score 281; DB 10; Length 686; Best Local Similarity 76.8%; Pred. No. 5.34e-165; Matches 251; Conservative 48; Mismatches 28; Indels (
                                                                        1 T;
                                                                        221 G;
                                                                        214 C;
                                                                                                                                                                                                                                                                                                                                                           IIIIIII I IIIII I ::IIIIIII CGCGGCCCC 327
                                                                        129 A;
                                                                         686 BP;
                                                                          Sequence
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Search completed: Mon Feb 23 20:51:53 1998 Job time: 64 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn Mon Feb 23 21:01:42 1998; MasPar time 23.30 Seconds 645.468 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-836-075A-1 (1-327) from USO8836075A.seq 317 Description:

1 ATGAGCACGAATCCTAAACC........CTCGGCCCAATTGGGGCCCC 327
TACTCGTGCTTAGGATTTGG.........GAGCCGGGTTAACCCCGGGG Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD: Nmatch

87531 seqs, 22996021 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued Database: Mean 7.562; Variance 4.432; scale 1.706 Statistics:

1:backl 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.									6.39e-179	
	Applicat	Applicat								
Description	Sequence 114,	Sequence 113,	Sequence 110,	Sequence 117,	Sequence 118,	Sequence 115,	Sequence 111,	Sequence 112,	Sequence 105, P	Sequence 124.
£	PCT-US95-1	PCT-US95-1								
DB	13	13	13	13	13	13	13	13	13	13
Query Match Length DB	573	573	573	573	573	573	573	573	573 13	573
Query Match	89.9	89.9	89.3	9.88	98.6	98.6	88.6	88.0	88.0	88.0
Score	285	285	283	281	281	281	281	279	279	279
Result No.		7	m	4	3	9	7	œ	6	10

/home/fuller/feb1098/US-08-836-075A-1.mi Feb 23 20:59

6.39e-179 6.39e-179	6.39e-179	3.37e-178	1.78e-177	1.78e-177	1.78e-177	1.78e-177	1.78e-177	4.95e-176	4.95e-176	4.95e-176	4.95e-176	4.95e-176	2.61e-175	1.38e-174	1.38e-174	3.83e - 173	3.83e-173	3.83e-173	2.02e-172	2.96e-170	8.20e-169	8.20e-169		8.20e-169	20e-	8.20e-169	4.32e-168	4.32e-168	3.32e-165	4.83e-163	2.54e-162	_	2.14e-154
Sequence 120, Applicat Sequence 108, Applicat	121,	106,	123,	104,	m	ฑ้	6,	116	122,	103,	119,	109,		Sequence 1, Applicatio	 Applicatio 	11, Applicati	Ξ,	14,	11, A	142,	17, A	17, Applicati	15, Applicati	15, Applicati	13,	13,	139,	145,	140,	141,	143,	151,	Sequence 150, Applicat
PCT-US95-1 PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US95-1	US-08-143-	US-08-143-	PCT-US91-0	PCT-US95-1			US-07-681-	PCT-US95-1	US-07-910-	PCT-US95-1	0	ı			0	US-07-681-	PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US95-1	PCT-US95-1		PCT-US95-1 Sequ						
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11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

APPLICANT: BURH, 3., MILLER, R.H. AND
APPLICANT: BURCELL, R.H.
TITLE OF INVENTION: MICLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIACNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263 PCT-US95-10398-114 STANDARD; DNA; UNC; 573 BP. Sequence 114, Application PC/TUS9510398. Sequence 114, Application PC/TUS9510398 GENERAL INFORMATION: ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM PC COMPATIBLE CORRESPONDENCE ADDRESS: CITY: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10154 01-JAN-1900 XXXXX RESULT

SOFTWARE:

TOPOLOGY:

Aome/fuller/feb1098/US-08-836-075A-1.mi Feb 23 20:59

Application PC/TUS9510398

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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAGGACGAATGCTAAACCTCAAAGAAAACGAAAGGTAACGCAACGCGGCCCTCAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 2.94e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homosapiens
INDIVIDUAL ISOLATE: P10
Sequence 573 BP; 96 A; 185 C; 179 G; 113 T; 0 other;
                                                                           R.H.
NUCLEOTIDE AND DEDUCED
Sequence 113, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   ADDRESSEE; MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.9%;
Best Local Similarity 90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297; Conservative
                                                                                             TITLE OF INVENTION: 1
TITLE OF INVENTION: 2
TITLE OF INVENTION: 3
TITLE OF INVENTION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                          STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 421792
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10154
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RESULT ID PC AC xx DT 01

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9 1 ATGAGCACGAATCCTAAACCTCAAAGACAAACCAAACGTAACACCCAACGCCCCCACAG 60 Gaps ö Length 573; 4; Mismatches 27; Indels Sequence 573 BP; 95 A; 189 C; 177 G; 112 T; 0 other; Score 283; DB 13; Pred. No. 8.21e-182; 545 573 base pairs 89,3%; ORGANISM: homosapiens INDIVIDUAL ISOLATE: S STRANDEDNESS: single Best Local Similarity 90.5%; Matches 296; Conservative nucleic acid TOPOLOGY: linear ORIGINAL SOURCE: Query Match

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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED T 4 PCT-US95-10398-117 STANDARD; DNA; UNC; 573 BP. APPLICANT: BUKH, J., MILLER, R.H. AND Sequence 117, Application PC/TUS9510398. Sequence 117, Application PC/TUS9510398 GENERAL INFORMATION: ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE TITLE OF INVENTION: NUCLEOT TITLE OF INVENTION: AMINO 1 TITLE OF INVENTION: CORE GITTLE OF INVENTION: SEQUENCES: 263 CORRESPONDENCE ADDRESS: 01-JAN-1900 XXXXXX

COMPUTER READABLE FORM: STATE: NEW YORK NEW YORK COUNTRY: USA ZIP: 10154

OPERATING SYSTEM: PC-DOS/MS-DOS MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE

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                                              APPLICANT: BURH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF TI
TITLE OF INVENTION: CORE GENES OF ISOLATES OF
TITLE OF INVENTION: AND THE USE OF REAGENTS DI
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC MI
NUMBER OF SEQUENCES: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/10398
Sequence 118, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
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APPLICATION NUMBER: 08/290/665
                                                                                                                                                                                                                                                                                              ADDRESSEE: MORGAN & FINNEGAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
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TELEFAX: (212) 751-6849
TELEX: 421792
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MEDIUM TYPE: FLOPPY DISK
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INDIVIDUAL ISOLATE: IN
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Best Local Similarity 90.2%;
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
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Pred. No. 2.29e-180;
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TITLE OF INVENTION: NUCLEOTIDE AND DEDUCTITLE OF INVENTION: CORE GENES OF ISOLATITLE OF INVENTION: CORE GENES OF REACES TITLE OF INVENTION: SEQUENCES IN DIAGNOSTITLE OF INVENTION: SEQUENCES IN DIAGNOSTITLE OF INVENTION:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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                                                           TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 90.2%;
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CORRESPONDENCE ADDRESS:
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                                                                                                        TOPOLOGY: linear
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Pred. No. 2.29e-180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches 28;
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTONEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
RECISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION:
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            APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995
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Sequence 112, Application PC/TUS9510398
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
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TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                       LENGTH: 573 base pairs
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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Local Similarity 90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295; Conservative
                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                             CLASSIFICATION:
                                                                                                                                                                                                                                                        TELEX: 421792
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APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
APPLICANT: PURCELL, R.H. REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800 APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995 CLASTEICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/086,428 FILING DATE: 29 JUNE 1993 OPERATING SYSTEM: PC-DOS/MS-DOS PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/290/665 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK FILING DATE: 15 AUGUST 1994 ATTORNEY/AGENT INFORMATION: COMPUTER: IBM PC COMPATIBLE INFORMATION FOR SEQ ID NO: 112: SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK TELEFAX: (212) 751-6849 US6 LENGTH: 573 base pairs SEQUENCE CHARACTERISTICS ORGANISM: homosapiens INDIVIDUAL ISOLATE: U NAME: RICHARD W. BORK CORRESPONDENCE ADDRESS: STRANDEDNESS: single TITLE OF INVENTION: PTITLE OF INVENTION: PTITLE OF INVENTION: CTITLE OF INVENTION: PTITLE OF TYPE: nucleic acid TOPOLOGY: linear STATE: NEW YORK TELEX: 421792 ORIGINAL SOURCE: COUNTRY: USA ZIP: 10154 a ð ð

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OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
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                      241 TACCCTTGGCCCCTCTATGGCAACGAGGCATGGGGTGGGCAGGATGGCTCCTGTCACCC 300
121 GGCCCCAGGNNGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCACAACCTCGTGGC 180
                                                                                                                                                                                                                                                                       NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                 PCT-US95-10398-105 STANDARD; DNA; UNC; 573 BP
                                                                                                                                                                                                                                                  APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUC TITLE OF INVENTION: AMINO ACID SEQUENCES TITLE OF INVENTION: CORE GENES OF ISOLATITLE OF INVENTION: SEQUENCES IN DIAGNOS TITLE OF INVENTION: SEQUENCES IN DIAGNOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2026-4116
                                                                                                                                                                                                                 Sequence 105, Application PC/TUS9510398. Sequence 105, Application PC/TUS9510398
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                          301 CGCGCTCTCGGCCCAATTGGGGCCCC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/086,428
                                                                                                               301 CGTGGCTCCCGGCCTAGTTGGGGCCCC 327
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : (212) 758-4800
(212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                    345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW YORK
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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BUKH, J., MILLER, R.H. AND

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VENTION: NUCLECTIDE AND DEDUCED
VENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
VENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
VENTION: AND THE USE OF REACENTS DERIVED FROM THESE
VENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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Pred. No. 6.39e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
                                                                                                                                                                                      ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 202 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15 AUGUST 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EX3
                                                                                                                                                                                                            345 PARK AVENUE
                                                                                                                                      NUMBER OF SEQUENCES: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.0%;
Best Local Similarity 89.9%;
Matches 294; Conservative
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                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                  CITY: NEW YORK STATE: NEW YORK
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                                                                                                                                                  Sequence 573 BP; 95 A; 184 C; 178 G; 116 T; 0 other;
                                                                                                                                                                                                                 Pred. No. 6.39e-179;
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Best Local Similarity 89.9%;
Matches 294; Conservative
                                                                                                        ORGANISM: homosapiens
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                                                                                 ORIGINAL SOURCE:
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ö 61 GACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCGGG 120 GCCCTAGATTGGGTGTGCGCGGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGT 180 TITLE OF INVENTION: AMINO PAGE SQUENCES OF THE ENVELOPE 1 AND TITLE OF INVENTION: OORE GENES OF ISOLATES OF HEPATITIS C VIRUS TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 263 1 ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGTCGCCCACAG 60 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCTCAK 60 Gaps ö Score 278; DB 13; Length 573; Pred. No. 3.37e-178; Indels Sequence 573 BP; 97 A; 182 C; 177 G; 117 T; 0 other; 4; Mismatches 29; R.H. NUCLEOTIDE AND DEDUCED REFERENCE/DOCKET NUMBER: 2026-4116 APPLICATION NUMBER: PCT/US95/10398 OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION: ADDRESSEE: MORGAN & FINNEGAN COMPUTER: IBM PC COMPATIBLE 36,459 TELEX: 421792 INFORMATION FOR SEQ ID NO: 106: TELECOMMUNICATION INFORMATION SOFTWARE: WORDPERFECT 5.1 (212) 758-4800 (212) 751-6849 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK FILING DATE: 15-AUG-1995 SHI 345 PARK AVENUE CURRENT APPLICATION DATA: LENGTH: 573 base pairs Query Match 87.7%; Best Local Similarity 89.9%; Matches 293; Conservative SEQUENCE CHARACTERISTICS NAME: RICHARD W. BORK ORGANISM: homosapiens CORRESPONDENCE ADDRESS: STRANDEDNESS: single REGISTRATION NUMBER: INDIVIDUAL ISOLATE: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TYPE: nucleic acid TOPOLOGY: linear STATE: NEW YORK NEW YORK COUNTRY: USA ORIGINAL SOURCE: ZIP: 10154 TELEPHONE: TELEFAX: STREET: 121

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Sequence 573 BP; 93 A; 183 C; 180 G; 117 T; 0 other; Alginal Course ORGANISM: homosapiens ORIGINAL SOURCE:

Gaps ö Length 573; 4; Mismatches 30; Indels Score 277; DB 13; 1 Pred. No. 1.78e-177; Query Match 87.4%; Best Local Similarity 89.6%; Matches 293; Conservative

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121 GCCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGATCGCAACCTCGTGGC 180 염

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241 CACCCTTGGCCCCTCTATGCCAATGAGGGCTTGGGGTGGGCGGGATGGCTCCTGTCACCC 300 g

301 ceceecreceeccraerreegecec 327 셤

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301 CGCGCCTCTCGCCCCAATTGGGGCCCC 327

Search completed: Mon Feb 23 21:02:08 1998 Job time : 26 secs.

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Feb 23 20:52:18 1998; MasPar time 208.41 Seconds 774.811 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-075A-1
Description: (1-327) from US08836075A.seq
Perfect Score: 317
N.A. Sequence: 1 ATGAGGAGGATCCTAAACC........CTGGGCCCCAATTGGGGCCCC 327

Comp: TACTCGTGCTTAGGATTTGG......GAGCCGGGTTAACCCCGGGG

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 665703 seqs, 246912890 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: ES

1:EST 2:EST 3:EST 4:EST 4:EST 6:EST 6:EST 7:EST 8:EST 8
9:EST 9 10:EST 10 11:EST 11 12:EST 12 13:EST 13 14:EST 14
15:EST 15 16:EST 16 11:EST 11 12:EST 12 13:EST 13 14:EST 14
15:EST 12 12:EST 23:EST 23 24:EST 24:EST 29:EST 25 26:EST 26
21:EST 22 22:EST 23:EST 23 24:EST 24:EST 25 26:EST 26
23:EST 23 34:EST 23 25:EST 23 34:EST 33:EST 33:ES

99:EST99 100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 110:EST109 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST120 121:EST120 121:EST120 121:EST120 121:EST120 121:EST120 121:EST120 122:EST120 120:EST120 120:EST120 120:EST120 120:EST120 120:EST120 120:EST120 120:EST130 120:EST130 130:EST130 13

Database:

133:EST134 135:EST135 136:EST136 137:EST137 138:EST138 139:EST139 140:EST140 141:EST141 142:EST142 143:EST143 144:EST144 145:EST145 146:EST146 147:EST147 148:EST148 149:EST149 149:EST149 149:EST149 149:EST149 149:EST159 153:EST153 154:EST156 153:EST153 154:EST159 160:EST160 161:EST150 157:EST157 158:EST158 169:EST169 160:EST160 161:EST161 162:EST167 168:EST168 169:EST169 170:EST170 171:EST177 172:EST172 173:EST173 174:EST179 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST189 190:EST189 190:EST190 191:EST191 192:EST192 193:EST193 194:EST194 195:EST195 196:EST199 196:EST195 196:EST199 196:EST199 196:EST199

Statistics: Mean 9.769; Variance 2.141; scale 4.562

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	.30e-05 .86e-04 .86e-04	.43e-03 .43e-03	2.43e-03 2.43e-03 2.43e-03 2.43e-03	2.43e-03 2.43e-03 89e-02 89e-02 89e-02 2.89e-02	2.89e-02 2.89e-02 2.89e-02 2.89e-02 2.89e-02	2.89e-02 2.89e-02 2.89e-02 2.89e-02 2.89e-02	2.89e-02 2.89e-02 2.89e-02 3.10e-01 3.10e-01 3.10e-01 3.10e-01 3.10e-01
Description P	ye52h03.s1 Homo sapie 1 yi75d01.s1 Homo sapie 1 yu27q08.s1 Homo sapie 1 yq43d01.s1 Homo sapie 1	sl Homo sapie 2 lomo sapiens c 2 sl Homo sapien 2	Homo sapie 1 Soares mou 1 Beddington Homo sapie	homo sapie 1 Soares fet Homo sapie Homo sapiens a transcrib 1 Stratagene Homo sapie	Homo sapiens Homo sapie Homo sapie Homo sapie	rl Homo sapie sl Homo sapie rl Homo sapie rl Homo sapie rl Homo sapie	zb70all.sl Soares fet mi20f11.rl Soares mou y019q12.rl Homo sapie 2.co70cl2.rl Stratagene ys67e06.sl Homo sapie 3.cp6302.sl Stratagene md44d04.rl Soares fet md44d04.rl Soares fet ze82b02.sl Soares fet
			R07673 AA038712 AA119984 H81577	90 93			N93628 AA028338 H46973 AA155686 H84640 AA181878 AA022461 W53431
Length DB	423 13 301 36 426 92 491 54	215 28 217 85 227 55	304 14 332 140 404 147 419 92			426965	482 121 514 138 514 46 81 170 331 93 345 180 345 180 342 158
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Score	22 22 22 22 22 22 22 22 22 22 22 22 22	21 21 21 21	21 21 21 21 21 21 21 21 21 21 21 21 21 2	20 20 20 20 20 20 20	50 50 50 50 50 50 50 50 50 50 50 50 50 5	20 20 20 20 20 20	20 20 20 19 19 19 19
Result No.	0 0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	-/		13 13 14 15 16 17 19	c 20 c 22 23	c 25 c 27 c 28 30	c 33 33 34 34 37 38 39 39

9 6.0 431 186 W84502 zh53a02.rl Soares fet 3.10e-01 9 .6.0 -442 92 H79035 yul.sg01.sl Homo sapie 3.10e-01 9 6.0 462 125 W12927 mb20g11.rl Soares mou 3.10e-01 9 6.0 470 43 R21500 yg06g10.rl Homo sapie 3.10e-01 9 6.0 493 160 W87973 mf65a07.rl Soares mou 3.10e-01 9 6.0 512 169 AA015386 mh15d07.rl Soares mou 3.10e-01	96691 423 bp mRNA 96501 96501 175515 175515 ST. uman clone=121397 library=Soares fetal ector=pTTT3D (Pharmacia) with a modifie ampicillin resistant) primer=-21ml3 Rsi iver and splean from a 20 week-post con trand cDNA was primed with a Pac I - ol ACTGCAAGAATTAATTAACATCTTTTTTTTTTTTTTTTT	Query Match 7.3%; Score 23; DB 13; Length 423; Best Local Similarity 70.5%; Pred. No. 1.30c-05; Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
40 19 c 41 19 · 42 19 · 44 19 c 45 19 c	RESULT 1 LOCUS DEFINITION 955 ACCESSION 7955 ACCESSION 7955 NEWMORDS EST: SOURCE Need (amp CANNIA Live Stra AACT CONSIDER HOME CONSIDER HOME AUTHORS HILL AUTHORS Tree Tree JOURNAL URPHORS AUTHORS AUT	Query Match Best Local Sin Matches 31;

(Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsitel=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygli, Choanata, Tetrapoda, Amniota, Mammalia, Theria, ö This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. human clone=145057 library=Soares placenta Nb2HP vector=pT7T3D Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,W., Kuczba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and 06-JUN-1995 09-NOV-1995 Gaps Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 ; 0 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 22; DB 36; Length 301; Pred. No. 1.86e-04; Indels EST 301 bp mRNA EST yi75d01.s1 Homo sapiens cDNA clone 145057 3'. R77276 LOCUS H79148 426 pp minns DEFINITION yu27g08.sl Homo sapiens cDNA clone 235070 3' ACCESSION H79148 5. 53 t 0; Mismatches /organism="Homo sapiens" High quality sequence stops: 276 Source: IMAGE Consortium, LINL 127 g Location/Qualifiers Email: est@watson.wustl.edu Wilson, R. The WashU-Merck EST Project Contact: Wilson RK WashU-Merck EST Project /clone="145057 26 c Query Match 6.9%; Best Local Similarity 84.4%; Matches 27; Conservative Unpublished (1995) Tel: 314 286 1800 Homo sapiens 65 a g1057237 EST. q851908 RESULT 2 LOCUS DEFINITION ACCESSION m source ORGANISM BASE COUNT TITLE JOURNAL REFERENCE AUTHORS KEYWORDS SOURCE FEATURES COMMENT ORIGIN RESULT NID g ð

KEYWORDS

238 CGGCTGAGCCCAGGACCTGCCCTCGGCGTTGGGG 195 165 cgggctgagaccccgtcctgcctgatgcaggccaggnttgggg

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source DEFINITION ORGANISM BASE COUNT JOURNAL Matches REFERENCE AUTHORS ACCESSION KEYWORDS SOURCE FEATURES COMMENT ORIGIN RESULT LOCUS OIN g. 셤 human clone=198529 primer=Promega -21m13 library=Soares fetal liver spleen 1NFLS vector=pT773D (Pharmacia) with a modified polylinker human clone=235070 primer=Promega -21m13 library=Soares fetal live host-DH10B (ampicillin resistant) Rsitel-Pac I Rsite2-Eco KI Liver and spleen from a 20 week-post conception male fetus. 1st strand host=DH10B (ampicillin resistant) Rsitel=Pac I Rsite2=Eco RI Liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarinini; Hominidae; Homo. R94705 491 bp mRNA EST 31-AUG-1995 yq43d01.s1 Homo sapiens cDNA clone 198529 3' similar to contains MER1 repetitive element ;. and spleen from a 20 week-post conception male fetus. 1st strand This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. 214 GAGGGCAGGTCCTGGGCTCAGCCCGGTATCCTTGGCCCTCTATGGCAATGAGGGCTGC 273 286 gagggcaggtctggggaccagtgcggggaagcttgggccccttgtgccaggtacgcctgc 345 0; Mismatches 19; Indels 0; Gaps 1 (bases 1 to 426)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 22; DB 92; Length 426; cDNA was primed with a Pac I - oligo(dT) primer [5' 3 others constructed by Bento Soares and M.Fatima Bonaldo. Washington University School of Medicine Pred. No. 1.86e-04; 107 t /organism="Homo sapiens" High quality sequence stops: 281 Source: IMAGE Consortium, LLNL 127 g Location/Qualifiers Email: est@watson.wustl.edu The WashU-Merck EST Project Unpublished (1995) /clone="235070" WashU-Merck EST Project 93 c Query Match 6.9%; Best Local Similarity 68.3%; Contact: Wilson RK 41; Conservative <1..>426 Fax: 314 286 1810 1..426 Homo sapiens Wilson, R. q973435 R94705 EST. source DEFINITION ORGANISM BASE COUNT Matches TITLE JOURNAL mRNA. ACCESSION REFERENCE AUTHORS KEYWORDS SOURCE FEATURES COMMENT ORIGIN SOURCE

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home/fuller/feb1098/US-08-836-075A-1.rsta

human clone=38147 library=Soares infant brain 1NIB vector=Lafmid BA host-DH10B (ampicillin résistant) primer-Promega -21m13 Rsitel-Not I Rsite2-Hind III Whole brain from a 73 days post natal female. 1st I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. ö Deuterostomia, Chordata, Vertebrata; Gnathostomata, Osteichthyes; Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. normalization. Library constructed by Bento Soares and M.Fatima I (bases I to 491)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 22-MAY-1995 Gaps Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 the Lafmid BA vector. Library went through one round of ;; 0 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 22; DB 54; Length 491; Pred. No. 1.86e-04; 10 others 2; Mismatches 12; Indels EST 215 bp mRNA EST yq66e02.s1 Homo sapiens cDNA clone 38147 3'. R49453 390 tgggnccagtaccngtcccnggaccgggggggggttggggnt 430 233 TGAGCCCAGGACCTGGCCTCGGRCGRCGAGCCTTGGGGAT 193 Washington University School of Medicine 138 t /organism="Homo sapiens" Email: est@watson.wustl.edu High quality sequence stops: 317 Source: IMAGE Consortium, LIANL 120 g Location/Qualifiers The WashU-Merck EST Project /clone="198529" WashU-Merck EST Project Query Match 6.9%; Best Local Similarity 65.9%; 107 c Contact: Wilson RK 27; Conservative Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 <1..>491 Homo sapiens Homo sapiens 116 a Wilson, R. Bonaldo. q820351 ORGANISM

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EcoRI adaptors were ligated, followed by digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lambda 2AP Express vector=Lambda 2AP Express host=E. coli XL1-Blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rsitel=EcoRI Rsite2=XhoI mRNA was purified from human fetal hearts
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human clone=J9576 primer=TCCAAAGAATTCGGCACGAG library=Fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .MAGE Consortium (info@image.llnl.gov) for further information.
                                                     Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarthini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptor-primer. EcoRI adaptors were ligated, followed by diges with XhoI, for directional cloning into predigested lambda ZAP
                                                                                                  1 (bases I to 215)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.43e-03;
0; Mismatches 16; Indels 0;
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Source: IMAGE Consortium, LINL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 68.6%;
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                                                                                                                                                                                                                                                                                                      Unpublished (1995)
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Fax: 314 286 1810
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                                                                                                          REFERENCE
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Molecular Cardiology

human clone=199547 primer=Promega -21m13 library=Soares fetal liver spleen INFLS vector=pF773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand I and cloned into the Pac I and Eco RI sites of the modified pT/T3 ö vector. Library went through one round of normalization. Library Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 11-SEP-1995 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Gaps Banting Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel: 4169788758 Fax: 416978550 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 227)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 4444 Firest Park Parkway, Box 8501, St. Louis, MO 63108 ö Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Score 21; DB 85; Length 217; Pred. No. 2.43e-03; 2; Mismatches 14; Indels constructed by Bento Soares and M.Fatima Bonaldo, R97434 227 bp mRNA EST yq55h06.s1 Homo sapiens cDNA clone 199547 3'. R97434 120 egececteggecteeggacacaatagggtetgeggttggtgt 161 82 CGCCACCCGGNNNNNNACWCCMTGAGGGCGGCGTTGGTGT 41 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 46 /organism="Homo sapiens" High quality sequence stops: 201 Amail: liewcc@utcc.utoronto.ca. Source: IMAGE Consortium, LINL Location/Qualifiers 6 g Email: est@watson.wustl.edu The WashU-Merck EST Project /clone="J9576" .. University of Toronto Best Local Similarity 61.9%; c 29 26; Conservative <1..>217 Unpublished (1995) Fax: 314 286 1810 Tel: 314 286 1800 Homo sapiens Wilson, R. 40 g983094 Query Match source DEFINITION BASE COUNT Matches ORGANISM **PRNA** ACCESSION NID KEYWORDS SOURCE REFERENCE AUTHORS FEATURES COMMENT ORIGIN g 염

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AA038712 332 bp mRNA EST 28-AUG-1996 mi92c09.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 474064 5' similar to gb:X53476 Mouse mRNA for non-histone chromosomal protein HMG-14 (MOUSE);. Dubuque, T., double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by ö Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Gaps Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 (Pharmacia). Library went through one round of ö Score 21; DB 14; Length 304; Pred. No. 2.43e-03; 4; Indels /dev stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" Dr. Minoru Ko (Wayne State University). /clone_lib="Soares mouse p3NMF19.5" 0; Mismatches Seq primer: -28M13 rev2 from Amersham 101 Contact: Marra M/Mouse EST Project /organism="Mus musculus" Email: mouseest@watson.wustl.edu The WashU-HHMI Mouse EST Project High quality sequence stop: 187. 102 gggacatgagccaccacgccagcgca 129 298 GEGACAGGANCCGGCCACCGCA 271 Location/Qualifiers 5 /clone="474064" Query Match 6.6%; Best Local Similarity 85.7%; 1 (bases 1 to 332) 24; Conservative Unpublished (1996) <1..>332 Fax: 314 286 1810 Tel: 314 286 1800 1..332 Murinae; Mus. Mus musculus house mouse. Waterston, R. 83 a MGI:284808 AA038712 q1514121 source DEFINITION BASE COUNT ORGANISM Matches JOURNAL mRNA AUTHORS ACCESSION REFERENCE FEATURES KEYWORDS RESULT COMMENT ORIGIN SOURCE g G S

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matings, excluding embryos that had developed head folds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and all extraembryonic tisrues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                               mn34a10.rl Beddington mouse embryonic region Mus musculus cDNA clone 539802 5' similar to TR:G1236085 G1236085 LISCH7 ;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Beddington mouse embryonic region"
  Length 332;
                                             2; Indels
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Query Match 6.6%; Score 21; DB 140;
Best Local Similarity 92.0%; Pred. No. 2.43e-03;
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                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector to vector length is 425
Seq primer: -40ml3 ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL6 x DBA
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                                                                                           205 tcaaagaaaaaccatacgtaactcc 229
                                                                                                                  21 TCAAAGAAAACCAAACGTAACAC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH12S"
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                house mouse.
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JOURNAL
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human clone=239411 primer=Promega -21m13 library=Weizmann Olfactory
Epithelium vector=pBluescript SK- host=SOLR cells (kanamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resistant) Rsitel-EcoRI Rsite2-XhoI From 35 year old female. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recognition site and an 18 base poly dT sequence. For the 5' er
the synthesized cDNA termini were treated with T4 DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LINL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 ggaatgcaaacttcatgagggcagggttttggttttatgtattgttttacacccaggatt 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 419)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
                                                                                                                                                                                                                                                                                11-DEC-1995
                                                         Gaps
                                                                                                             44 ggtctagggatccacgtgctgaccccagatcccgtcagcgatcccacgatcctcggg 100
                                                                                                                                          252 GGCCAAGGATACCCGGGCTGAGCCTGCCCTGCGCCCTGGGCCTTGGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA was oligo (dT) primed with an XhoI restriction enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                      0;
Score 21; DB 147; Length 404;
Pred. No. 2.43e-03;
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                                                      1; Mismatches 18; Indels
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yu/3b06.s1 Homo sapiens cDNA clone 239411 3'.
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/clone="239411"
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                                                                                                                                                                                                                                                                           419 bp
Query Match 6.6%;
Best Local Similarity 66.7%;
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                                                      38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library ö Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 1 (bases 1 to 468)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
WashU-Merck EST Project Gaps Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. constructed by Bento Soares and M.Fatima Bonaldo." /clone="246590" DEFINITION 9171d11.s1 Homo sapiens CDNA clone 144693 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains TAR1 repetitive element ; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; home#uller/feb1098/US-08-836-075A-1_rsta 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 ö 246690 3' similar to contains Alu repetitive element;. /clone_lib="Soares fetal liver spleen INFLS" Query Match 6.6%; Score 21; DB 183; Length 468; Best Local Similarity 85.7%; Pred. No. 2.43e-03; Matches 24; Conservative 0; Mismatches 4; Indels /dev stage="20 week-post conception fetus" 9 others /lab_host="DH10B (ampicillin resistant) Washington University School of Medicine 94 t Insert Length: 634 Std Error: 0.00 /organism="Homo sapiens" High quality sequence stop: 86. Location/Qualifiers 271 TGCGGGGGGGGGGNTGGCTCCTGTCCC 298 11 tgcggctgggcgtggtggctcatgtccc 38 complement (<1..>468) 131 g RNA Seg primer: m13 -40 forward WashU-Merck EST Project 210 bp /sex="male" 103 c Contact: Wilson RK Unpublished (1995) Tel: 314 286 1800 Fax: 314 286 1810 1..468 Homo sapiens q1194314 131 R76212 human. R76212 Feb 23 20:52 source 14 ORGANISM TITLE JOURNAL BASE COUNT ACCESSION ACCESSION REFERENCE KEYWORDS FEATURES RESULT COMMENT ORIGIN SOURCE LOCUS

2

N I D KEYWORDS	9850894 EST.	(ampicillin resistant) primer=M13RP1 Relitel=Pac I Rel Liver and spleen from a 20 week-post conception male
SOURCE	human clone=144693 library=Soares placenta Nb2HP vector=pT7T3D (Pharmacia) with a modified notylinker host=DH1OR (ampicillin	strand cDNA was primed with a Pac I - oligo(dT) prime AACTGGAAGAATAAATAAAGATCTTTTTTTTTTTTTTTT
		CDNA was ligated to Eco RI adaptors (Pharmacia), dige
	placenta obtained at birth (full term). Ist strand cDNA was primed with a Not I - oligo(dT) primer [5,	I and cloned into the Pac I and Eco KI sites of the m vector. Library went through one round of normalizat
	AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTT	
	CDNA was ingated to Eco KI adaptors (Fnarmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3	UKUANISM HOMO Sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
	vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo	Deuterostomia; Chordata; Vertebrata; Gnathostomata; O Sarcopteryqii; Choanata; Tetrapoda; Amniota; Mammalia
ORGANISM	Homo sapiens	
	Eukaryotae; Metazoa; Eumetazoa; Bliateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcontervoii: Choanata: Tetranoda; Amniota: Mammalia: Theria:	REFERENCE 1 (Dases 1 to 2/6) AUTHORS Hillier, L., Clark,N., Dubuque,T., Elliston,K., Hawkin AUTHORA Hillier, L., Clark,N., Kucaba,T., Le.M., Lennon,G.,
o contraction	Eutheria Archonta, Primates; Catarrhini; Hominidae; Homo.	Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.
REFERENCE AUTHORS	<pre>1 (bases 1 to 210) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,</pre>	-
	Holman, M., Hultman, M., Kucaba, Y., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,	TILE The Mash-Merck EST Project JOURNAL Unpublished (1995)
	Trevaskis,E., Materston,R., Milliamson,A., Mohldmann,P. and Wilson,R.	COMMENT Contact: Wilson RK
TITLE	The WashU-Werck EST Project Unpublished (1995)	WashU-Merck EST Project Washington University School of Medicine
COMMENT	Contact: Wilson RK	4444 Forest Park Parkway, Box 8501, St. Louis, MO 651 Tel: 314 286 1800
	WashU-Merck EST Project	Fax: 314 286 1810
	Masnington University school of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Endall: escewatson.wust.edu High quality sequence stops: 267
	Tel: 314 286 1800	. INII damard conf
	rax: 514 con 1610 Email: est@watson.wustl.edu	
	High quality sequence stops: 185	FEATURES Location/Qualifiers
	Source: ITANE CONSOLLIME, DANE This clone is available royalty-free through LINL ; contact the	source 110 /organism="Homo sapiens"
	IMAGE Consortium (info@image.llnl.gov) for further information.	/clone="191840"
FEATURES	Location/Qualifiers 1210	38 g 62 C
	/organism="Homo sapiens" /clone="144693"	
BASE COUNT ORIGIN	33 a 66 c 84 g 23 t 4 others	Best Local Similarity 83.3%; Pred. No. 2.89e-02; Matches 25; Conservative 0; Mismatches 5; Indels 0
Query Mate	Query Match 6.3%; Score 20; DB 35; Length 210;	Db 197 tttaatttgaggtttatgattcttgctgat 226
Matches		Cp 30 TTTCTTCAGGTTTAGGATTCTGCTGTT 1
Db 14 cc	cccatggcaaaggcagcggggggggggggggggggggctgccggggc 68	Sparsh completed. Mon Eah 23 20.58.03 1998
Çıy 252 CC	252 CCTCTATGGCATGAGGCTGCGGGGGGGGGGTGGCTCCTGTTCTCTGTGTGGTGG	Job time: 225 secs.
T 15	# 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	
DEFINITION	10-80105.rl Homo sapiens CORA clone 191840 5. similar to physpole05.rl Homo sapiens CORA clone 191840 6. similar to physpole10HUMALNE34 Human carcinoma cell-derived Alu RNA cranscript, (RRNA); gb:D25272 !!!! ALU CLASS A WARNING ENTRY !!!!	
ACCESSION NID KEYWORDS	(HOTHAN); . H40395 191647 EST.	
SOURCE	human clone=191840 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B	

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Gaps

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iver and spleen from a 20 week-post conception male fetus. 1st trand cDNA was primed with a Pac I - oligo(dT) primer [5' ACTGCAACAATTAATTAAAGATCTTTTTTTTTTTTTTT], double-stranded DNA was ligated to Eco RI adaptors (Harmacia), digested with Pac and cloned into the Pac I and Eco RI sites of the modified pT7T3 ector. Library went through one round of normalization. Library nostructed by Bento Soares and M.Fatima Bonaldo. uterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; rcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; theria; Archonta; Primates; Catarrhini; Hominidae; Homo. is clone is available royalty-free through LLNL; contact the AGE Consortium (info@image.llnl.gov) for further information. mpicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI (bases 1 to 276)
Llier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., slman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., rsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., evaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and ashington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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ax: 314 286 1810
axis setewatson.wustl.edu
anil: estewatson.wustl.edu
anil: maliky sequence stops: 267
ource: IMAGE Consortium, LINL karyotae; Metazoa; Eumetazoa; Bilateria; Coelomata; 2 others 82 t /organism="Homo sapiens" 58 g Location/Qualifiers e WashU-Merck EST Project shU-Merck EST Project /clone="191840 59 c ntact: Wilson RK published (1995) mo sapiens

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm

Mon Feb 23 20:56:26 1998; MasPar time 121.28 Seconds 760.423 Million cell updates/sec MPsrch nn Run on:

Tabular output not generated.

>US-08-836-075A-1 (1-327) from USO8836075A.seq 317 Description: Perfect Score:

1 ATGAGCACGAATCCTAAACC......CTCGGCCCAATTGGGGCCCC 327 N.A. Sequence:

Tactcgtgcttaggatttgg......gagccgggttaaccccggg TABLE default Gap 6 Scoring table:

Comp:

397346 seqs, 141010104 bases x 2

Dbase 0; Query 0

STD:

Nmatch

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

LEST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202 7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208 13:EST209 14:EST204 9:EST205 10:EST206 11:EST207 12:EST208 13:EST209 14:EST210 15:EST210 17:EST213 18:EST209 14:EST212 0:EST212 21:EST213 2:EST213 24:EST213 24:EST213 25:EST213 25:EST213 25:EST213 25:EST223 24:EST223 27:EST223 27:EST223 27:EST223 27:EST223 27:EST223 27:EST223 27:EST223 27:EST233 27:EST234 27:EST235 27:EST236 27:EST236 27:EST236 27:EST236 27:EST238 27:EST238 27:EST239 27:EST239

Database:

99:EST295 100:EST296 101:EST297 102:EST298 103:EST299 104:EST300 105:EST301 106:EST302 107:EST303 108:EST309 109:EST305 110:EST305 1112:EST309 113:EST309

/home/fuller/feb1098/US-08-836-075A-1.rstb Feb 23 20:55

114:EST310 115:EST311 116:EST312 117:EST313 118:EST314 119:EST315

Mean 9.703; Variance 2.133; scale 4.548 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			;		
No.	Score	Match	Length	8	ID	Description	Fred. No.
	22	i٠	226	i	AA282971	zt14a08.sl Soares NbH	
2	22	6.9	326	42	PD03	sapiens EST sequ	9.16e - 05
e			353		AA395721	3 Lambda-P	
6	2	6.9	458	116	AA454719	zx77b02.sl Soares ova	9.16e-05
c 5		9.9	309		AA231797	RZ630.F cDNA from ric	1.20e - 03
9	•	9.9	369	S	AA004946	.s1 So	1.20e - 03
7		9.9	389		AA073040	ī.	$\overline{}$
80			421	œ	3725	.sl Soare	$\overline{}$
6			427	9	AA126152	.r.	$\overline{}$
1	-		450	81	1065	zt29q04.rl Soares ova	1.20e-03
c 11			473		AA402119	r.	1.20e-03
c 12			216	61	314	T.	1.44e - 02
c 13		•	259		AA396794	.rl Soares	
14			291		AA076835	chr	1.44e - 02
15		•	312	9	AA403843	.rl Soare	1.44e - 02
c 16	20		331	67	AA409505	£	1.44e - 02
17			358		210	.r1	1.44e - 02
c 18			378	82	AA428428	zv48c12.rl Soares ova	1.44e - 02
19			382	-	AA147251	r.	1.44e - 02
20			415		AA290473	vb37a07.rl Soares mou	1.44e - 02
c 21	20	6.3	433		AA080174	.rl Stratag	1.44e - 02
2		6,3	435	-	AA278629	.rl Soares	1.44e - 02
c 23			453		AA215509	97b06.rl Soares	1.44e - 02
7		6.3	473	35	AA147482	1	1.44e - 02
25			200	-	AA271194	r.	1.44e - 02
c 26	1	•	133		AA233407	.rl Strata	1.56e-01
27	1	•	161	-	AA261679	Soares m	1.56e-0
c 28	1	•	171	Ξ	AA449928	01.rl Soares	1.56e-
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8	19	0.9	255		AA337037	Endometria	•
c 31	-		271		AA353160	Activated T	•
c 32	-		284	4	AA340074	4 Fetal skin	1.56e - 01
	7		306		AA078095	Chromosom	•
c 34	1		340		AA330985	Embryo,	r.
32	-		341		AA32107	:=	ഹ
c 36	1	0.9	348		AA4559	aal6g06.sl Soares NhH	;
c 37	-	•	355	-	9	S	ഗ
38			362		RICC1690A	NA, part	1.56e-01
e	7	•	380		AA349543	3 In	•
c 40			330	7	AA243729	.81	1.56e - 01
41	1	0.9	410	79	AA402016	zu53b11.81 Soares ova	1.56e - 01
c 42	1		4	104	HUM103G04B	fetal	
c 43	-		448	99	AA403509	Barstea	1.56e - 01
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ALI GNMENTS

RESULT

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ORGANISM BASE COUNT TITLE Matches AUTHORS AUTHORS REFERENCE AUTHORS ACCESSION REFERENCE REFERENCE JOURNAL KEYWORDS KEYWORDS FEATURES TITLE COMMENT RESULT ORIGIN SOURCE SOURCE 셤 ð Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of formalization, and was /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; let strand cDNA was prepared from germinal B-cells (flow-sorted from tonsils) provided by Dr. Louis Standt of the NCI, and was then primed with a Not I - oligo(dT) primer [5' ö I (bases I to 226)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, E., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. AA282971 226 bp mRNA EST 15-MAY-1997 tt14a08.s1 Soares NbHTGBC Homo sapiens CDNA clone 713078 3'. Gaps 21-APR-1997 constructed by Bento Soares and M. Fatima Bonaldo." H.sapiens EST sequence (007-X3-17) from skeletal muscle. F19292 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 ö 126 tccctggtccatctctggtgaggacggctgggagtgggctctgtggcgct 176 Score 22; DB 98; Length 226; Pred. No. 9.16e-05; 0; Mismatches 15; Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 220. Location/Qualifiers Washington University School of Medicine /tissue_type="Germinal B-cell" 58 t /clone lib="Soares NbHTGBC" /organism="Homo sapiens" complement (<1..>226) a 56 c 70 g Email: est@watson.wustl.edu /lab host="DH10B" Contact: Wilson RK WashU-Merck EST Project 326 bp Query Match 6.9%; Best Local Similarity 70.6%; 36; Conservative Unpublished (1997) 1..226Homo sapiens a HSPD03892 g1925885 AA28297. human. Нопо. EST. 7 source DEFINITION ORGANISM DEFINITION BASE COUNT TITLE JOURNAL Matches ACCESSION ACCESSION mRNA AUTHORS REFERENCE KEYWORDS FEATURES COMMENT ORIGIN SOURCE g 3

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Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G. Identification of 4,370 expressed sequence tags (ESTs) from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sonicated and size selected (450-550 BP). The biotinylated 3'-ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were affinity purified, directionally cloned and sequenced (5' ->
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-DEC-1995) CRIBI Biotechnology Centre, University of
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Padua, Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA395721 353 bp mRNA EST 25-APR-1997
28123 Lambda-PRL2 Arabidopsis thaliana cDNA clone 40B12XP 3',
AA395721
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                                                                                                                                                                                                                                            3'-end specific cDNA library of human skeletal muscle by DNA
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/sex="female"
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 9.16e-05;
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Genome Res. 1, 35-42 (1996)
2 (bases 1 to 326)
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Best Local Similarity 70.5%;
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RE_2: NotI
                         Homo sapiens
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adapters (Pharmacia), digested with Not I and cloned into ö Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and 27-FEB-1997 Gaps Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; Oryza. Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 ; 0 AA231797 309 bp mRNA EST 27-RZ630.F cDNA from rice Oryza sativa cDNA clone RZ630. AA231797 Score 22; DB 116; Length 458; Pred. No. 9.16e-05; /tissue type="ovarian tumor" /lab host="DH10B (ampicillin resistant)" complement(<1...>458) 2; Mismatches 11; Indels 165 cgggctgagacccggtcctgcctgatgcaggccaggattgggg 208 238 CGGGCTGAGCCCAGGACCTGCCCTCGGRCCGRCGAGCCTTGGGG 195 /clone_lib="Soares ovary tumor NbHOT" /sex="Female" Seq primer: -41m13 fwd. ET from Amersham 94 t /organism="Homo sapiens" High quality sequence stop: 406. /db_xref="GDB:6039448" _126 c 145 g Location/Qualifiers M.Fatima Bonaldo." /clone="809739" 6.98; Best Local Similarity 70.5%; 31; Conservative Fax: 314 286 1810 Tel: 314 286 1800 Oryza sativa 93 a g1854169 rice. Query Match source DEFINITION ORGANISM BASE COUNT Matches ACCESSION FEATURES KEYWORDS COMMENT SOURCE ORIGIN RESULT LOCUS S, g

VanDeynze, A.E., Sorrells, M.E., Park, M.D., Ayres, N.M., Fu, H., Cartinhour, S.W. and McCouch, S.R.

(bases 1 to 309)

AUTHORS

REFERENCE

Anchor Probes for Comparative Mapping of Grass Genera

Unpublished (1997)

TITLE JOURNAL

Cornell University Ithaca, NY 14853-1901, USA

Unpublished (1997)

JOURNAL

TITLE

Dept Plant Breeding Contact: McCouch SR

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home/fuller/feb1098/US-08-836-075A-1.rstb Feb 23 20.55

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptee, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library This is a subtracted version of the original Soares fetal 1st strand cDNA was primed ö mm78b02.rl Stratagene mouse embryonic carcinomaRA (#937318) Mus musculus cDNA clone 534507 5' similar to TR:G1236085 G1236085 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 07-FEB-1997 Gaps constructed by Bento Soares and M.Fatima Bonaldo." /clone_lib="Soares fetal liver spleen lNFLS S1" Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 ö Score 21; DB 50; Length 369; Pred. No. 1.20e-03; /dev_stage="20 week-post conception fetus" 3 others 0; Mismatches 14; Indels 179 tggtggagtggagcaggtgccttgcaggaggcccagtgaggaggtgc 225 93 TGGTGGAGTTTACCTGTTGCCGCGCAGGCCCCCAGGNNGGCTGTGC 139 /lab_host="DH10B (ampicillin resistant)" with a Pac I - oligo(dT) primer [5' EST Washington University School of MedicineP liver spleen 1NFLS library. 95 t Contact: Marra M/Mouse EST Project organism="Homo sapiens" Email: mouseest@watson.wustl.edu The WashU-HHMI Mouse EST Project /db_xref="GDB:1328067" 120 g mRNA complement (<1..>369) WashU-HHMI Mouse EST Project Location/Qualifiers /clone="428298" 389 bp /sex="male" Query Match 6.6%; Best Local Similarity 70.2%; Matches 33; Conservative 77 c Unpublished (1996) Mus musculus Waterston, R. house mouse. æ AA073040 AA073040 q1594770 LISCH7 source DEFINITION BASE COUNT ORGANISM mRNA AUTHORS JOURNAL ACCESS ION REFERENCE KEYWORDS

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mRNA Matches JOURNAL AUTHORS ACCESSION REFERENCE KEYWORDS FEATURES TITLE COMMENT ORIGIN SOURCE 셤 ð /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. PI9 cell line treated with retinoic acid. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA ö Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Watersten, R. and Wilson, R. Washu-Merck EST Project 1997 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 291. AA437253 421 bp mRNA EST 30-MAY-1997 zv54e08.sl Soares testis NHT Homo sapiens cDNA clone 757478 3' AA437253 Gaps /dev stage="RA-treated P19 cell line (ATCC CRL1825)"
/lab_host="SOLR (kanamycin resistant)" /clone lib="Stratagene mouse embryonic carcinomaRA (#9373<u>1</u>8)" 252 GGGCCAAGGATACCCGGGCTGAGCCCAGGACCTCGCCCTCGGRCCACCATGGG 196 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 204 ggtctagggatccacgtgctgaccccagatcccgtcay.gatcccacgatcctcggg ö 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' Score 21; DB 9; Length 389; 1; Mismatches 18; Indels MGI:321443 Seq primer: -28ml3 revl ET from Amersham. Washington University School of Medicine Pred. No. 1.20e-03; CTCGAGTTTTTTTTTTTTTT 3'" 69 /organism="Mus musculus" /organism="Homo sapiens" 117 g Location/Qualifiers Location/Qualifiers Email: est@watson.wustl.edu /clone="534507" WashU-Merck EST Project 6.68; Best Local Similarity 66.7%; 105 c (bases 1 to 421) Conservative Contact: Wilson RK Unpublished (1997) Tel: 314 286 1800 Fax: 314 286 1810 Homo sapiens q2142167 86 human. 38; Query Match source source DEFINITION ORGANISM EASE COUNT TITLE JOURNAL Matches ACCESS ION REFERENCE AUTHORS KEYWORDS FFATURES FEATURES COMMENT

SOURCE

ORIGIN

g, g

/home/fuller/feb1098/US-08-836-075A-1.rstb

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was
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                           Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                         Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@imago.llnl.gov) for further information. Insert Length: 2041 Std Error: 0.00
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EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2185h07.rl Stratagene colon (#937204) Homo sapiens cDNA clone 511453 5' similar to TR:G451854 ALPHA-WANNOSIDASE ;. AA126152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., Wash U-Werck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1997
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                                                                                                                                                                                      constructed by Bento Soares and M. Fatima Bonaldo.
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was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 89; Length 421;
Pred. No. 1.20e-03;
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                                                                                                                                                                                                                                                             /clone lib="Soares testis NHT"
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                                                                                                                                                                                                                                                                                                                                          complement (<1..>421)
/db_xref="GDB:5978092"
1 122 c 151 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 gctgggccgagggcacgtcctgggcacag 405
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                                                                                                                                                                                                                                                                                                                                                                                           151 g
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                                                                                                                                                                                                                                                                                                                 /lab host="DH10B"
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                                                                                                                                                                                                                                                                                        /sex="male"
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                                                      primer (5'
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ORIGIN

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Feb 23 20:55

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/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/clone="723798"
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                   sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
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                                             insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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0
       Oligo dT. T-84 colonic epithelial cell line.
                                                                                                                                                                                     /clone_lib="Stratagene colon (#937204)"
/lab host="SOLR cells (kanamycin resistant)"
<1...5427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 427;
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_125 c 147 g
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                                                                                                                                                                      /clone="511453"
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SOURCE

/organism="Homo sapiens"

source

COMMENT

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo."

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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pP7T3 vector
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5' similar to TR:G397579 G397579 LL5 MRNA. ;.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
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Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                             Score 21; DB 81; Length 450;
Pred. No. 1.20e-03;
                                                                                                                            2 others
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
\.7450
/db_xref="GDB:5935183"
135 c 144 g 83 t ? othore
                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28m13 rev2 ET from Amersham

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                      234 CTGAGCCCAGGACCTGCCCTCGGRCCGRC 206
                                                                                                                                                                                                                                                                                                                          273 ctgtgcccaggacgtgccctcggcccage 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 bp
                                                                                                                                                                                                               Query Match 6.6%;
Best Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 473)
                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..473
```

/tissue_type="ovarian tumor" /lab_host="DH10B (ampicillin resistant)"

/sex="Female"

29 t

2 others 41 a

BASE COUNT

Score 20; DB 61; Length 216; Pred. No. 1.44e-02; 0; Mismatches 12; Indels Query Match 6.3%; Best Local Similarity 72.1%; 31; Conservative Query Match Matches

313 GCCGAGAGCCGCGGGGGACAAGAGCCANCCCGCCCACCGCGA 271 g g DEFINITION vb28h10.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone Accession AA396794

g2049801

KEYWORDS

Murinae; Mus.

REFERENCE

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Homo sapiens

ORGANISM

human.

AA031467 g1501533 470696 5'

ACCESSION

KEYWORDS

DEFINITION

RESULT

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

(bases 1 to 216)

REFERENCE AUTHORS Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

JOURNAL

TITE

AA031467 216 bp mRNA EST 09-MAY-1997 zk16c05.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone

AUTHORS

Waterston, R.

Contact: Marra M/Mouse EST Project

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:459291

vector to vector length is 260 Seg primer: -28ml3 rev2 ET from Amersham.

/organism="Mus musculus" /strain="C57BL/6J"

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer $\{5'$ 3']; double-stranded cDNA was ligated to Eco RI adaptors

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTT 3'],

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization.

constructed by M. Fatima Bonaldo."
/clone="470696"

/clone_lib="Soares pregnant uterus NbHPU"

/sex="female"

/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'

/organism="Homo sapiens"

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 936 Std Error: 0.00

Email: est@watson.wustl.edu

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 188.

Location/Qualifiers

source

FEATURES

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Washington University School of Medicine

WashU-Merck EST Project

Contact: Wilson RK

normalized by Bento Soares and M.Fatima Bonaldo.

/clone="750307"

Feb 23 20:55

/dev_stage="adult" /lab_host="DH108" <l..516 /db_xref="GD8:3756698" a 92 c 52 g 6

ORIGIN

22 gccgggcccagtgggagagcagcagccagccaccccca 64

ö

Gaps

; 0

4; Indels

Score 21; DB 79; Length 473;

85 t

147 g

ø

88

BASE COUNT

ORIGIN

/db_xref="GDB:5942137" _153 c 147 g

<1..>473

Pred. No. 1.20e-03;

Query Match 6.6%; Best Local Similarity 82.8%;

24; Conservative

Matches

1; Mismatches

234 CTGAGCCCAGGACCTGCCCTCGGRCCGRC 206

260 ctgtgcccaggacgtgccctcggcccagc 288

4 Cb

ö

Gaps

ö

house mouse,

SOURCE

ORGANISM

Mus musculus

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

1 (bases 1 to 259)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

The WashU-HHMI Mouse EST Project

Unpublished (1996)

WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Putative full length read

Location/Qualifiers 1..259 FEATURES

source

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D. 2,006 Expressed-Sequence Tags Derived from Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting direct-selected cDNA was cloned into a plasmid
vector using a non-directional uracil DNA glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selection using chromosome 7 genomic DNA (cosmids). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: brain; Vector: pAMP10; cDNA was generated
                                                                                                                                                                                                                                                                                                                                                   AA076835 291 bp mRNA EST 08-OCT-1996
7B03F10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens CDNA
clone 7B03F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 7-enriched cDNA was isolated by direct cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hexamers and oligo(dT). From this pool of cDNA, human
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from cytoplasmic RNA using a mixture of random DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Chromosome 7 Fetal Brain cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                           114 accaccactggagaaggaactctttcaaggccatggtttgtgttctgttgggg 166
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                    1; Mismatches 20; Indels
                                                                                                                                                             Length 259;
/clone_lib="Soares mouse lymph node NbMLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="pool of 9 week and 12 week" /lab_host="E. coli strain DH5 alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UDG)-mediated cloning strategy." /clone="7B03F10"
                                                                                                                                                                                Pred. No. 1.44e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female and male mixture"
                                                                                                                                                               DB 65;
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                                                                                                                                                               Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: egreenθnhgri.nih.gov
Plate: 03 row: F column: 10
Seq primer: -21M13 (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="brain"
                                      /dev_stage="4 weeks"
/lab_host="DH108"
                                                                                               61 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Eric D. Green
                     /sex="male"
                                                                                                                                                                                  Best Local Similarity 60.4%;
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g1836309
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home/fuller/feb1098/US-08-836-075A-1,rstb
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                                                             Score 20; DB 9; Length 291;
Pred. No. 1.44e-02;
                                                                                                0; Mismatches 10; Indels
                                                             Query Match 6.3%;
Best Local Similarity 75.0%;
Matches 30; Conservative
   Feb 23 20:55
                                                               Query Match
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I (bases I to 312)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                LOCUS AA403843 312 bp mRNA EST 29-APR-1997 DEFINITION vd79f11.rl Soares mouse NbMH Mus musculus cDNA clone 806829 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
237 ggccccaagnggggtgtgcgggtggatagcaggggttccg 276
                                   121 GCCCCCAGNNGGTGTGCGCGCGACTAGGAAGACTTCCG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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                                                                                                                                                                                                                                                                         AA403843
92057815
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Mayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima /note="Vector: pT7T3D-Pac (Pharmacia) with a modified Seq primer: -28ml3 rev2 ET from Amersham. /clone lib="Soares mouse NbMH" 65 /organism="Mus musculus" /tissue_type="heart" /dev_stage="4 weeks" /lab_host="DH108" Location/Qualifiers
1..312 5 /strain="C57BL/6J" 82 /clone="806829" /sex="male" 38 c Bonaldo." <1..>312 64 a source

; 0 Query Match 6.3%; Score 20; DB 66; Length 312; Best Local Similarity 72.2%; Pred. No. 1.44e-02; Matches 26; Conservative 2; Mismatches 8; Indels 0; Gaps

Search completed: Mon Feb 23 20:58:41 1998 Job time: 135 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

Mon Feb 23 20:59:06 1998, MasPar time 122.41 Seconds 673.945 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

Tabular output not generated.

(1-327) from USO8836075A.seq 317 >US-08-836-075A-1 Description:

Perfect Score: N.A. Sequence:

1 ATCAGCACGAATCCTAAACC.......CTCGCCCCAATTGGGCCCCC 327
TACTCGTGCTTAGGATTTGG........GAGCCGGGTTAACCCCGGGG Comp:

TABLE default Scoring table:

Gap 6

Dbase 0; Query 0 Nmatch STD

333433 seqs, 126143548 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

15.5121 2.5120 1.5151 11.5151 11.5120 1.5151 15.5150 1.5150 1.5150 1.5151 15.5150 1.51 1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8

Mean 9.719; Variance 2.202; scale 4.415 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

home/fuller/feb1098/US-08-836-075A-1.rstc Feb 23 20:58

and is derived by analysis of the total score distribution.

SUMMARIES

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Result	,	Query	:		;		
No.	Score	Match	Length	8	e	Description	Pred. No.
1	22		156	_	DM36D7S	D, melanogaster STS d	1.48e-04
2	22	6.9	226	52	187	114a08.sl NC	8e-0
m	22		226	22	AA282971	a08.81 NCI CGAP	8e-0
4	22		350	27	AA480207	sl NC	48e-
2	22	6.9	350	64	HS1271527	.sl NC	4
	22	6.9	458	78	-	sl So	1.48e - 04
	21		294	œ	G25421	TS EST40574	1.80e - 03
	21		341	79	HSAA64094	4.rl Soares o	80e-
	2		341	9	7	1	1.80e-03
3 .	3 5		419	9 0		TS SHGC-35139	809-0
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1 1	77 6		175	7,0	0717044311	.si Joanes	1 000 03
	77 7		775	0 5	00107WYCH	11 Stidlay	1.00-03
C 13	77		450	7	HS120/341	Soares	1.80e-03
	21		473	24	HS1201862	rl Soares or	
15	20		275	69	HS1300003	.rl NCI CGAP	
16	70	-	275	32	AA504541	aa60c02.rl NCI CGAP G	
17	20		291	95	HS1137730	Chromo	
18	20		358	96	MM1139801	1.	
19	20		378	57	HS1226722	rl Soares o	
	50		382	77	HSAA47251	.rl Soares	
7.5	<u>20</u>		393	72	HS1316949	sl NCI CGA	
22	20		393	42	AA525270	.s1 NCI CGAP	
33.	20		395	85	MM1295319	.rl Stratage	
24	20	6.3	395	34	AA4 988 68	7	2.00e-02
25	20		402	91	T09138	0	
	20		435	51	HS1182879	rl NCI CGAF	
	20		435	20	AA278629	.rl NC	
	20		453	16	HSAA38042	.rl NCI CGA	
	20		453	14	AA215509	.rl NCI CGAP	
	20		473	11	HSAA47482	50a05.rl Soares	
333	20		546	13		UT27.	
	10		146	22	AA282835	3.rl NCI CGA	.02e-
33	10		146	52	HS1187378	t15f03.rl NCI CGAP	.02e-
	5	0.9	306	5	HSAA78095	POIE12 Chromosome	
 	5 -		306	: =	HIJMSWS 3587	hromosome 7	02e-
	-		306	12	HTMSWS 3587	chromosome 7	.02e-
	2 2		355	;	AA281664	A r1 NCI CCAP	029-
	1 5		370	1 12	HS8083	eno sable	02e-
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	10		410	2 2	HS1201751	Spares	0.0
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ALIGNMENTS

	156 bp DNA STS 16-APR-1996	D. melanogaster STS determined from European Mapping Project				ite.	
	DM36D7S 156	D. melanogaster S	cosmid.	0880/2	g1263754	sequence tagged site.	fruit fly
RESULT 1	LOCUS	DEFINITION		ACCESSION	MID	KEYWORDS	SOTTRUE

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Increal Vector: pTT33-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lat strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Standt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer 31. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library wen through one round of normalization, and was constructed by ö Gaps ö 126 tecetggtecatetetggtgaggaeggetgggagtgggetgetgtggetget 176 Length 226; 0; Mismatches 15; Indels //tissue_type="germinal center B cell"
/lab_host="DH10B" Bento Soares and M. Fatima Bonaldo. Sequence 226 BP; 42 A; 56 C; 70 G; 58 T; 0 other; Score 22; DB 52; Pred. No. 1.48e-04; /clone lib="NCI CGAP GCB1" organism="Homo sapiens" complement (<1..>226) Best Local Similarity 70.68; 36; Conservative Query Match source mRNA Matches

AA282971 DEFINITION ACCESSION

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 13-JUN-1997 AA282971 226 bp mRNA EST 13-JUN-199 zt14a08.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone 713078 3'. (bases 1 to 226) Unpublished (1997) Tumor Gene Index Homo sapiens q1925885 NCI-CGAP human. See See ORGANISM REFERENCE AUTHORS JOURNAL

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Ecs RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman Email: Robert Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lange.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 220.
Location/Qualifiers /organism="Homo sapiens" Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 source

S

cDNA synthesis was

(NCI) and Dr. Gerald Marti (CBER).

Unpublished. NCI-CGAP; AA480207; Query Match q2208358 source 1 - 350BASE COUNT Matches RESULT ID HS ORIGIN g ð DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not ö and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, Gaps 19-JUN-1997 constructed by Bento Soares and M. Fatima Bonaldo." Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 0; Mismatches 15; Indels 0; ne30h02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 898899. AA480207 243 TCCTTGGCCCCTCTATGGCATGAGGGCTGCGGGGGGGGGCGCATGGCTCCT 293 126 tecetggtecatetetggtgaggaeggetgggagtgggetetgtggetget 176 Score 22; DB 22; Length 226; M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. /tissue_type="germinal center B cell" /lab_host="DH10B" cDNA Library Arraying: Greg Lennon, Ph.D. Seq primer: -41m13 fwd. ET from Amersham Pred. No. 1.48e-04; www-bio.llnl.gov/bbrp/image/image.html 58 t /clone="713078" /clone lib="NCI CGAP GCB1" /organism="Homo sapiens" Contact: Robert Strausberg, Ph.D. Email: Robert_Strausberg@nih.gov High quality sequence stop: 345. complement(<1..>226) 56 c 70 g Location/Qualifiers Query Match 6.9%; Best Local Similarity 70.6%; rel: (301) 496-1550 (bases 1 to 350) Conservative Tumor Gene Index Unpublished (1997) Homo sapiens NCI-CGAP. AA480207 g2208358 42 human. 36; Ношо. DEFINITION source ORGANISM BASE COUNT

ACCESSION

KEYWORDS

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL

FEATURES

Matches

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ORIGIN

home/fuller/feb1098/US-08-836-075A-1_rstc

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polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed
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                                 modified pTTT3 vector. Library went through one round of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert Strausbergenth, gov Tissue Procurement: Elias Campo, M.D., Michael R. Empert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone
I and cloned into the Not I and Eco RI sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     distribution: NCI-CGAP clone distribution information can be found
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 27; Length 350;
Pred. No. 1.48e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 15; Indels
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23-JUN-1997 (Rel. 52, Last updated, Version 1)
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/clone_lib="NCI_CGAP_
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/lab_host="DH108"
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/note=*Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNAwas size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                 07-JUN-1997 (Rel. 52, Created)
07-JUN-1997 (Rel. 52, Last updated, Version 1)
2x77b02.s1 Soares ovary tumor NbHOT Homo sapiens CDNA clone 809739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             est@watson.wustl.edu This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wylle T., Waterston R., Wilson R.; "WashU-Merck EST Project 1997";
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                                                                                                                                                             243 TCCTTGGCCCCTCTATGGCAATGAGGGCTGCGGGGTGGGCGGGGTTCCT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Rominidae; Homo.
                                                          Query Match 6.9%; Score 22; DB 64; Length 350; Best Local Similarity 70.6%; Pred. No. 1.48e-04; Matches 36; Conservative 0; Mismatches 15; Indels
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Pred. No. 1.48e-04;
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/clone_lib="Soares ovary tumor NDHOT"
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Sequence 458 BP; 93 A; 126 C; 145 G; 94 T; 0 other;
mRNA <1...>350
Sequence 350 BP; 71 A; 96 C; 128 G; 55 T; 0 other;
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Key Location/Qualifiers
                                                                                                                                                                                                                                  LT 6
HSAAS4719 standard; RNA; EST; 458
AA454719;
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Best Local Similarity 70.5%;
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Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                              31-MAY-1996
                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotee; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
                                                                                                                                                                                     STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Romo sapiens"
/map="48.5 cR from top of Chr14 linkage group"
1..150
                                                                                                                                                                                                                                                                                                                                                                                                                           Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA
                                    238 C3GGCTGAGCCCAGGACCTGCCCTCGGRCGAGCCTTGGGG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derived from dbEST (genbank accession H81577).
                                                                                                              STS
165 cgggctgagacccgtcctgcctgatgcaggcaggattgggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taq Polymerase: 0.025 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer A: ACAAAATATTACCACCCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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                                                                                                            G25421 294 bp
human STS EST405749.
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Tris-HCL: 10 mM
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MgCl2: 1.5 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presoak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STS size: 150
                                                                                                                                                                                                                                              Homo sapiens
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primer_bind
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/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector
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                                                                (Pharmacia). Library constructed by Bento Soares and
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                                    Gaps
                                                                                                                                                                                                                                                                                    13-JUN-1997 (Rel. 52, Created)
13-JUN-1997 (Rel. 52, Last updated, Version 1)
2x82h04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 810295
5' similar to TR:G397579 G397579 LL5 MRNA. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        est@watson.wustl.edu This clone is available royalty-free through LIML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wyler T., Waterston R., Wilson R.; "WaahU-Merck EST Project 1997";
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 21; DB 8; Length 294;
Pred. No. 1.80e-03;
                                    2; Mismatches 22; Indels
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/lab_host="DH10B (ampicillin resistant)"
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/clone="810295"
/clone_lib="Soares ovary tumor NDHOT"
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70 A; 100 C; 109 G; 62 T; 0 other;
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1; Mismatches 4
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 Query Match 6.6%;
Best Local Similarity 61.5%;
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Matches 24; Conservative
                                    40; Conservative
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zx82h04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 810295 5' similar to TR:G397579 G397579 LL5 MRNA.;
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
/home/fuller/feb1098/US-08-836-075A-1.rstc
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Pred. No. 1.80e-03;
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/sex="Female"
                                                                                                                                                                                                             53
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    Mismatches

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                                                                             /db_xref="GDB:6040546"
_100 c 109 q
                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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259 ctgtgcccaggacgtgccctcggcccagc 287

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Prepared with primer pairs provided by Sandoz, derived from H81577 -- Washington University/Merck EST sequence.
                                                                          04-0CT-1996
                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 degrees C for 15 seconds
62 degrees C for 23 seconds
72 degrees C for 30 seconds
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                            Department of Genetics, M-344, Stanford, CA 94305, USA
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Pred. No. 1.80e-03;
                                                                          STS
                                                                                                                                  STS sequence; primer; sequence tagged site.
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Stanford University School of Medicine
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0.05 units/ul
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h 1 uM
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Primer B: TTTTATGTACCAATTGCTGAATG
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/map="14"
2.5 融
50 融
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                                                                                                                                                                                                                                                                                                                                                            Email: myers@shgc.stanford.edu
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Total Vol:
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                                                                         G29737 419 bp
human STS SHGC-35139.
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ORGANISM
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AUTHORS
JOURNAL
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                                                            RESULT
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6.68;

Query Match Best Local Similarity

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/note="Vector: p173D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                               46 ggaatgcaaacttcatgagggcagggttttggttttatgtattttacacccaggatt 105
                                                                                                                74 GGNNNNNNACWCCMTGAGGGGGGGGGGTT-GGTGTTACGTTTGGTTTTCTTTGAGGTTT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo." /clone="757478" /clone_lib="Soares testis NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          est@watson.wustl.edu This clone is available royalty-free through LIML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 291.

Location/Qualifiers

Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wylie T., Waterston R., Wilson R.;
home/fuller/feb1098/US-08-836-075A-1.rstc
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Pred. No. 1.80e-03;
1; Mismatches 4; Indels
                                            Indels
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                                                                                                complement (<1..>421)
BP; 75 A; 122 C; 151 G; 73 T; 0 other;
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01-JUN-1997 (Rel. 52, Last updated, Version 1)
                                            Mismatches
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                                             2;
                                                                                                /sex="male"
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Best Local Similarity 82.8%;
                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                  106 agaat 110
                                                                                                                                                                                   15 AGGAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 421
                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                         AA437253;
   Feb 23 20:58
                                                                                                                                                                                                                                                                                         g2142167
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                                               Matches
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/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Olig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dr. T-84 colonic epithelial cell line. Average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    est@watson.wustl.edu This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2041 Std Error: 0.00 Seq primer: -28Ml3 rev2 from Amersham High quality sequence stop: 240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK WashU-Merck EST Project Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                            z185h07.rl Stratagene colon (#937204) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                              511453 5' similar to TR: C451854 G451854 ALPHA-MANNOSIDASE ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hohman M., Hultman M., Kucaba T., Le M., Lemnon G., Marra M. Barsons J., Rikkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "Waahd-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Stratagene colon (#937204)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATTCGGCACGAG 3'~3' adaptor sequence:
CTCGAGTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 A; 125 C; 147 G; 76 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                  30-NOV-1996 (Rel. 50, Created)
24-MAY-1997 (Rel. 52, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism≃"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 ccctcaggtggtgctggccccgggtggcgg 248
                                     206 GYCGGYCCGAGGCCAGGTCCTGGGCTCAG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 CCCTCAKGGSGTNNNNNNCCGGGTGGCGG 83
377 gctgggccgagggcacgtcctgggcacag 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                HSAA26168 standard; RNA; EST; 427 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS1207341 standard; RNA; EST; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="511453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1997 (Rel. 51, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.6%;
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished,
                                                                                                                                                                                                                                               AA126152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA410657;
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Mome/fuller/feb1098/US-08-836-075A-1_rstc Feb 23 20:58

/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5] (Pharmacia). Library constructed by Bento Soares and Gaps est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High 01-MAY-1997 (Rel. 51, Created) 22-MAY-1997 (Rel. 52, Last updated, Version 2) zu55d04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 741895 23-MAY-1997 (Rel. 52, Last updated, Version 2) zt29g04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 723798 School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: ŝ Contact: Wilson RK WashU-Merck EST Project Washington University ö Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., Score 21; DB 54; Length 450; Pred. No. 1.80e-03; /tissue_type="ovarian tumor" /lab_host="DH10B (ampicillin resistant)" <1...>450 4; Indels /clone lib="Soares ovary tumor NbHOT" BP; 85 A; 135 C; 144 G; 83 T; 2 other; 5' similar to TR:G397579 G397579 LL5 MRNA. ;. White Y., Wylie T., Waterston R., Wilson R.; Mismatches organism="Homo sapiens" 234 CTGAGCCCAGGACCTGGCCTCGGRCCGRC 206 273 ctgtgcccaggacgtgccctcggcccage 301 ВЪ. Location/Qualifiers HS1201862 standard; RNA; EST; 473 AA402119; M.Fatima Bonaldo." "WashU-Merck EST Project 1997"; /clone="723798 /sex="Female" 6.68; quality sequence stop: 443. Best Local Similarity 82.8%; 24; Conservative (human) Homo sapiens (human) Homo sapiens Sequence 450 Unpublished Query Match source 1 - 450mRNA Matches RESULT
1D HS
AC AA
NI 92
DT 22
DE ZU
DE 5
CW E
CO E
CO E
CO E
CO E 염 ტ

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2

C Robert_Strausberg@nih.gov Tissue Procurement: Louis M. Staudt,

/note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M.Staudt (NCI), Dr. David Allman J. Double-stranded cDNA was ligated to Eco RI adaptors (through one round of normalization, and was constructed by and Eco RI sites of the modified pT7T3 vector. Library wen Pharmacia), digested with Not I and cloned into the Not I ö (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was Gaps M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Grey Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the www-bio.llnl.gov/bbrp/image/image.html Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 260. ö Score 20; DB 69; Length 275; Indels primed with a Not I - oligo(dT) primer /clone lib="NCI CGAP GCB1" /tissue type="germinal center B cell" Bento Soares and M. Fatima Bonaldo. Sequence 275 BP; 88 A; 43 C; 41 G; 103 T; 0 other; . 9 Pred. No. 2.00e-02; 0; Mismatches /organism="Homo sapiens" 16 AAACCTCAAAGAAAACCAAACGTAACACCAA 47 29 aaactgcaaagaaaaaccaaaaacaacaa 60 Location/Qualifiers /lab host="DH108" I.M.A.G.E. Consortium/LINL at: Best Local Similarity 81.3%; 26; Conservative Query Match source **MRNA** Matches

Search completed: Mon Feb 23 21:01:23 1998

Job time : 137 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPerch pp

Mon Feb 23 10:59:47 1998; MasPar time 6.00 Seconds 252.111 Million cell updates/sec Tabular output not generated.

Run on:

>US-08-836-075A-2 (1-109) from US08836075A.pep

781 Description: Perfect Score:

1 MSTNPKPQRKTKRNTNRRPX......GCGWAXWLLSPRGSRPNWGP 109 Sequence:

PAM 150 Scoring table:

111726 seqs, 13889129 residues Gap 11 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq30 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

Mean 28.686; Variance 128.255; scale 0.224 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	8.90e-62	2.12e-61	2.12e-61	2.12e-61	2.12e-61	2.12e-61	2.12e-61	3.27e-61	3.27e-61	3.27e-61	3.27e-61
		typ	typ	180	180	SR0	YS1	den	180	180	iso	180
		virus	virus	virus	virus	virus	virus	virus	virus	virus	virus	virus
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	Description	Hepatitis	Hepatitis	Hepatitis C v	Hepatitis	Heprtitis						
		526	539	R92976	973	591	589	588	. 116	937	939	941
	8	R96	R96	R92	R92	R67	R67	R67	R92	R92	R92	R92941
	03	19	13	11	11	12	12	12	11	11	11	11
	Query Match Length DB	109	117	191	191	505	502	3011	191	191	191	191
40	Query Match	100.0	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5
	Score	781	777	777	777	777	777	777	775	775	775	775
	Result No.		7	٣	4	'n	9	7	œ	60	10	==

3.27e-61	3.27e-61	3.27e-61	3.27e-61	3.27e-61	27e-	3.27e-61	3.27e-61	3.27e-61	3.27e-61	4.06e-61	7.77e-61	9.65e-61	9.65e-61	9.65e-61	1.20e - 60	1.20e-60	2.85e~60	2.85e-60	2.85e - 60	2.85e-60	2.85e-60	2.85e - 60	2.85e-60	2.85e-60	2.85e-60	2.85e-60	2.85e - 60	3.54e - 60	3.54e-60	4.40e - 60	4.40e - 60	4.40e - 60	4.40e-60
Hepatitis C virus iso	Hepatitis C Virus cor	Hepatitis C virus iso	pHCV141-encoded seque	HCV genome type la(H)			HCV sequence.	HCV genomic amino aci	HCV genomic amino aci	Hepatitis C virus iso	Hepatitis C virus typ	C virus	ပ	Hepatitis C virus iso	C virus	Hepatitis C virus iso	HCV C22 domain antige	Hepatitis C virus cor	p HCV-34 Hepatitis co	HCV CKS-Core pHCV34 a	HCV CKS-core - pHCV-3	HCV CKS-Core pHCV-34	Sequence of fusion pr	HCV CKS-Core fusion p	HCV-1 polyprotein.	Hepatitis C virus pol		HCV-Hc59 capsid and e	GST:NANBV 690:691 enc	Synthetic HCV nucleoc	Synthetic HCV nucleoc	eptide 2	Composite hepatitis C
R92940	R44010	R92938	R79222	W12715	R79221	R22154	R79232	R40119	R40120	R92974	R96531	R63374	R25123	R92936	R92978	R92972	R90936	R63359	R52689	R33631	R21564	R33593	R22207	R33573	R34009	R90931	R21519	R22137	R22145	R74047	24	5	R70230
	191 8						3011 13			191 17	319 19	166 12							396 10	396	396 4	396	396 4	396 6		3011 15				_	196 13		2894 13
99.5	99.2	99.5	99,2	99.5	99.5	99.5	99.5	99.5	99.5	99.1	98.7	98.6	98.6	98.6	98.5	98.5	0.86	0.86	0.86	0.86	98.0	0.86	0.86	0.86	98.0	98.0	98.0	8.76	8.76	7.76	7.76	7.76	7.76
775	775	775	775	775	775	775	775	775	775	174	171	170	770	770	169	169	765	765	765	765	765	765	765	765	765	765	765	764	754	763	763	763	763
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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07-WAR-1997 (first entry)
Hepatitis C virus type 1d isolate BNL1 amino acids 1-103.
Hepatitis C virus; subtype; polymerase chain reaction; amplification; PCR; primer; probe; antibody; infection.
                                                                                                                                                                                           /note= "amino acid in this position is designated X in the specification, but codon usage shows that the only possible amino acid at this pos. is Gly" Misc difference 22
                                                                                                                                                                                                                                                                       /note= "amino acid in this position is designated X in
                                                                                                                                                                                                                                                                                       the specification, but codon usage shows that the only possible amino acid at this pos. is Val Misc_difference 23.
                                                                                                                       Location/Qualifiers
 LT 1
R96526 standard; peptide; 109 AA.
                                                                                                                                                                                                                                                                                                                                                Misc difference 24
/label= any amino acid
Misc difference 44
                                                                                                                                                                                                                                                                                                                                   /label= any amino acid
                                                                                                                                   Misc difference 20
/label= His, Gln
                                                                                                                                                               Misc_difference 21
/label= Gly
                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                         /label= Val
                              R96526;
RESULT
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/label= any amino acid

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hepatitis C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-j, 5a and 6a. They esp. from the novel subtypes 1d-f_1 2e-j, 2k, 21, 3g, 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5' untranslated region (9R), the Croe/E1, Nsf or NSSB regions of the genome. This sequence represents amino acids 1-103 from the HCV type 1d isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplified, cloned and genotyped. The 5'UR, Core/El and NS5B regions were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The new HCV types were isolated from patients with chronic HCV from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 mstnpkpgrktkrntnrrpxxxxxxpgggqivggvyllprrgprxgvratrktsersqprg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection of HCV in a sample. The polypeptides can be used to detect anti-HCV antibodies, for HCV typing or to prevent HCV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences R96526-R96578 represent novel sequences isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses into (sub)types based on comparison with known sequences. The sequences were used to generate the peptides R96424-R96524. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus poly:nucleic acid unique to unidentified sub:type

    used to develop probes and primers for new sub:types and vaccines

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequenced either directly or partially and used to classify the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences can also be used to synthesise probes and primers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benelux countries, France, Cameroon and Vietnam, because of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 781; DB 19; Length 109;
Pred. No. 8.90e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 rrqpipkaxrxegrswaqpgypwplygnegcgwaxwllsprgsrpnwgp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus type 4k isolated BNL7 amino acids 1-117.
                                                                                                                                                                                                          /note= "amino acid in this position is designated X in
                                                              /note= "amino acid in this position is designated X in
                                                                                 the specification, but codon usage shows that the
                                                                                                                                                                                                                              the specification, but codon usage shows that the
                                                                                                       only possible amino acid at this pos. is Arg
                                                                                                                                                                                                                                                   only possible amino acid at this pos. is Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R96539 standard; peptide; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; Fig 3; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to prevent and treat infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109; Conservative
                                                                                                                                                                                                                                                                                                              23-0CT-1995; E04155.
21-0CT-1994; EP-870166.
28-JUN-1995; EP-870076.
                                                                                                                                                                                                                                                                                                                                                                              (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                      Stuyver L;
                     Misc difference 69
                                                                                                                        difference 71
                                                                                                                                                                 Misc difference 95
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 96-251460/25.
                                                                                                                                            /label= Ala, Pro
                                                                                                                                                                                                                                                                         WO9613590-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T2793
                                                                                                                                                                                                                                                                                            09-MAY-1996.
                                                                                                                                                                                       /label= Gly
                                            /label= Arg
                                                                                                                                                                                                                                                                                                                                                                                                      Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R96539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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Claim 25; Fig 3; 150pp; English.

The sequences R96526-R96578 represent novel sequences isolated from hepatitis C virus subtypes different from subtypes la-c, 2a-d, 3a-f, 4a-j, 5a and 6a. They esp. from the novel subtypes l-f, 2e-j, 2k, 2l, 3g, 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5' untranslated region (UR), the Core/El, NS4 or NS5B regions of the genome. This sequence represents amino acids 1-117 from the HCV type 4k isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The 5'UR, Core/El and NS5B regions were sequenced either directly or partially and used to classify the new viruses into (sub)types based on comparison with known sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus isolate 26 core protein.
HCV; El; envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSTNPKPQNKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                         Hepatitis C virus poly:nucleic acid unique to unidentified sub:type - used to develop probes and primers for new sub:types and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences were used to generate the peptides R96424-R96524. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 mstnpkpqrktkrntnrrpmdvkfpgggqivggvyllprrgprlgvratrktsersqprg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benelux countries, France, Cameroon and Vietnam, because of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-HCV antibodies, for HCV typing or to prevent HCV infections
Aome/fuller/feb1098/US-08-836-075A-2.rag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 rrqpipkarrsegrswaqpgypwplygnegcgwaxwllsprgsrpswgp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 777; DB 19;
Pred. No. 2.12e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                   PCR; primer; probe; antibody; infection.
                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä.
                                                                                                                                                                                                                                                                                                                                                                   to prevent and treat infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 3
R92976 standard; Protein; 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R92976;
02-0CT-1996 (first entry)
                                                                                                                             /note= "any amino acid" W09613590-A2.
                                                                                                                                                                                    23-0CT-1995; E04155.
21-0CT-1994; EP-870166.
                                                                                                                                                                                                                                                (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                            28-JUN-1995; EP-870076.
                                                                                                                                                                                                                                                                    Maertens G, Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1995; U10398.
                                                                                                           Misc difference 95
                                                                                                                                                                                                                                                                                     WPI; 96-251460/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
                                                                        Hepatitis C virus.
                                                                                                                                                                                                                                                                                                           N-PSDB; T27950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9605315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1996.
                                                                                                                                                                  09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
 Feb 23 10:57
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(USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH.

Hepatitis C virus; subtype; polymerase chain reaction; amplification;

15-AUG-1994; US-290665.

Anme/fuller/feb1098/US-08-836-075A-2 rag

Feb 23 10:57

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                                                                            used to determine HCV genotype and as vaccines against HCV infection Claim 4; Page 214; 340pp; English.
R92936-R92987 are HCV core proteins derived from 52 different HCV
                                                                                                                                      isolates. Isolated cDNA sequences are used for the prodn. of primers
                                                                                                                                                                                                                                                                                                                                                                                           1 mstnpkpgrktkrntnrrpmdvkfpggggivggyllprrgprlgvratrktsersgprg 60
                                                                                                                                                                                                                                                                                                                                                                                                                 HCV; E1; envelope 1; core protein; HCV genótyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolates. Isolated cDNA sequences are used for the prodn. of primers
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                proteins may also be used to detect antibodies against HCV in serum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins may also be used to detect antibodies against HCV in serum,
                                                                                                                                                                                                                                 saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection. Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    saliva, lymphocýtes or other mononuclear cells. The antibodies may
be used in the prevention of HCV infection.
Sequence 191 AA;
                                                                                                                                                          useful for detecting the presence of HCV in a sample, the primers
                                                                                                                                                                            are also useful for HCV genotyping. Proteins encoded by the cDNAs
                                                                                                                                                                                                can be used in vaccines for immunising against HCV infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used in vaccines for immunising against HCV infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R92936-R92987 are HCV core proteins derived from 52 different HCV
                                      N-PSDB; T16650.

DNA and amino acid sequence of HCV envelope 1 and core proteins
                                                                                                                                                                                                                                                                                                                                                       •
                                                                                                                                                                                                                                                                                                             Score 777; DB 17; Length 191;
Pred. No. 2.12e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus isolate 28 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-1995, U10398.

15-AUG-1994; US-290665.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

(USSH ) US SEC DEPT HEALTH.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R92973 standard; Protein; 191 AA.
 Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purcell RH;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-0CT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                       99; Conservative
Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukh J, Miller RH, WPI; 96-139709/14.
 Bukh J, Miller RH, WPI; 96-139709/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T16647,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatitis.
                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                     Matches
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1 mstnpkpqrktkrntnrrpqdvkfpgggqivggvyllprrgprmgvratrktsersqprg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           079143 is the hepatitis C virus (HCV) gene SR037-5' cDNA, it encov
the protein described in R67591. Both the cDNA and protein can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A hepatitis C virus gene and oligo-nucleotide(s) - used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A hepatitis C virus gene and oligo-nucleotide(s) - used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                               61 rrqpipkarrsegrawaqpgypwplygnegcgwagwllsprgsrpswgp 109
                                                                                                                                Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 rrqpipkarrpegrswaqpgypwplygnegcgwagwllsprgsrpswgp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RROP I PKAXRXEGRSWAOP GYPWP LYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; non-A non-B; SR037-5'; treatment.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; non-A non-B; YS117-5'; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.5%; Score 777; DB 12; 90.8%; Pred. No. 2.12e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus SR037-5' gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in the treatment of HCV infection Sequence 502 \ \mathrm{AA};
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Claim 19; Pagg 34; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page 36; 41pp; Japanese.
                                                                                                                                                                                                                                                                                     R67591 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 6
R67589 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.8%;
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-1994.
13-MAY-1993; 147133.
13-MAY-1993; JP-147133.
(IMMO) IMMUNO JAPAN KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMO ) IMMUNO JAPAN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1993; JP-147133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1993; 147133.
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Indels

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1; Mismatcher

Score 777; DB 17; Length 191;

Pred. No. 2.12e-61;

Query Match . 99.5%; Best Local Similarity 90.8%;

99; Conservative

1 mstnpkpqrktkrntnrrpmdvkfpgggqivggvyllprrgprlgvratrktsersqprg 60

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                                                                                                                                                             1 MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Pages 21-33; 41pp; Japanese. Q79140 is the hepatitis C virus (HCV) gene HC-G9 cDNA, it encodes the protein described in R67588. Both the cDNA and protein can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A hepatitis C virus gene and oligo-nucleotide(s) - used for the
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Pred. No. 2.12e-61;
  Length 502;
                                                                                                                                                                                                                  61 rrqpipkarrpegrswaqpgypwplygnegcgwagwllsprgsrpswgp 109
                                                                                                                                                                                                                                             61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
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                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus gene product HC-G9.
Hepatitis C virus; HCV; non-A non-B; HC-G9; treatment.
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Score 777; DB 12;
Pred. No. 2.12e-61;
                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             R67588 standard; Protein; 3011 AA.
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99.5%;
90.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc difference 2506..2565
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                                                         99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of hepatitis C
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                              Best Local Similarity
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22-NOV-1994.
13-MAY-1993; 147133.
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  Query Match
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HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolates. Isolated cDNA sequences are used for the prodn. of primers
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                                                                                                                                                                                                                                                                                             used to determine HCV genotype and as vaccines against HCV infection
                                                                                                                                                                                                                                                                                                                                                                                        useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolates. Isolated cDNA sequences are used for the prodn. of primers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are HCV core proteins derived from 52 different HCV
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                                                                                                                                                                                                                                                                    DNA and amino acid sequence of HCV envelope 1 and core proteins -
                                                                                                                                                                                                                                                                                                                                            R92936-R92987 are HCV core proteins derived from 52 different HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA and amino acid sequence of HCV envelope 1 and core proteins
/home/fuller/feb1098/LUS-08-836-075A-2 rag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 775; DB 17;
Pred. No. 3.27e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used in the prevention of HCV infection. Sequence 191 AA;
                                                                                                                 15-AUG-1994, US-290665.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES. (USSH ) US SEC DEPT HEALTH.
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                                                                                                                                                                                            Miller RH, Purcell RH;
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Best Local Similarity 89.9%;
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15-AUG-1995; U10398.
15-AUG-1994; US-290665.
                                                                                          15-AUG-1995; U10398,
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N-PSDB; T16611.
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                                                                                                                                                                                                                                          N-PSDB; T16651.
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      Feb 23 10:57
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                                                                                                                                                                                            Bukh J,
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proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection.

Sequence

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                                                                                                                                                                                                                                                                                                    02-OCT-1996 (first entry)
Hepatitis C virus isolate SW1 core protein.
HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                              1 MSTNPKPORKTKRNTNRRPXXXXXPGGGOIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to determine HCV genotype and as vaccines against HCV infection
                                                                           1 mstnpkpqrktkrntnrrpqdvkfpgggqivggvyllprrgprlgvratrktsersqprg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolates. Isolated cDNA sequences are used for the prodn. of primers
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Sequence 191 AA;
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 183; 340pp; English.
R92936-R92987 are HCV core proteins derived from 52 different HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be used in vaccines for immunising against HCV infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA and amino acid sequence of HCV envelope 1 and core proteins
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   Length 191;
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Pred. No. 3.27e-61;
                                                                                                                                                                      61 RRQPIPKAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPWWGP 109
                                                                                                                                                   61 rrqpipkarrpegrtwaqpgypwplygnegcgwagwllsprgsrpswgp 109
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                                    9; Indels
Score 775; DB 17;
Pred. No. 3.27e-61;
                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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15-AUG-1994; US-290665.
(USSH ) US DEPT HEALTH 6 HUMAN SERVICES.
(USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                 R92939 standard; Protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukh J, Miller RH, Purcell RH; WPI; 96-139709/14.
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Best Local Similarity 89.9%;
 99.2%;
89.9%;
                                        98; Conservative
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                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                hepatitis.
 Query Match
                                                                                                                                                                                                                                                                                      R92939;
                                        Matches
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Hepatitis C virus isolate S18 core protein. HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; R92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunishing against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, Bukh J, Miller RH, Purcell RH; WPI; 96-139709/14.
N-PSDB; T11614.
Name a maino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection 1 MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRG 60 used to determine HCV genotype and as vaccines against HCV infection isolates. Isolated cDNA sequences are used for the prodn. of primers Gaps can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of HCV infection. Sequence 191 AA; saliva, lymphocytes or other mononuclear cells. The antibodies may 1 mstnpkpqrktkrntnrrpqdvkfpggqivqgvyllprrgprlgvratrktsersqprg useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs R92936-R92987 are HCV core proteins derived from 52 different HCV DNA and amino acid sequence of HCV envelope 1 and core proteins -; 0 Length 191; 61 rrqpipkarrpegrtwaqpgypwplygnegcgwagwllsprgsrpswgp 109 9; Indels Score 775; DB 17; Pred. No. 3.27e-61; 2; Mismatches be used in the prevention of HCV infection. (USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH. (USSH) US DEPT HEALTH & HUMAN SERVICES. (USSH) US SEC DEPT HEALTH. Claim 4; Page 184-185; 340pp; English. Claim 4; Page 184; 340pp; English. Ą. Purcell RH; JT 12 R92940 standard; Protein; 191 99.28; Best Local Similarity 89.9%; 98; Conservative 02-0CT-1996 (first entry) 15-AUG-1994; US-290665. 15-AUG-1995; U10398. 15-AUG-1994; US-290665. Miller RH, 15-AUG-1995; U10398 WPI; 96-139709/14. N-PSDB; T16615. Hepatitis C virus. WO9605315-A2. 22-FEB-1996. hepatitis. Sequence Query Match Bukh J, R92940; Matches 19 염 임 ð δ

Hepatitis C virus isolate DR4 core protein. HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;

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R92941 standard; Protein; 191

02-0CT-1996 (first entry)

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R92941;

Hepatitis C virus.

hepatitis.

1 mstnpkpgrktkrntnrrpqdvkfpggggivggvyllprrgprlgvratrktsersqprg 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Of peptides 1-3 (see Features Table), peptide 1 was found to be from the immunodominant region of HCV core protein. Further analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the N-terminal 45 amino acids of the HCV core protein showed that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            some epitopes are present in the first 21 amino acids, some in 22-45
                              Gaps
                                                                                                                                                                                                                                        Hepatitis C Virus core protein.
HCV; non-A, non-B hepatitis virus; NANBHV; immunodominant region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-353383/45.
New antigenic polypeptide(s) from hepatitis C virus - derived
from N-terminal region of core protein, and related antibodies,
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                           ;`
Score 775; DB 17; Length 191; Pred. No. 3.27e-61;
                                                                                                            61 rrqpipkarrpegrtwaqpgypwplygnegcgwagwllsprgsrpswgp 109
                                                                                                                         Score 775; DB 8; Length 191; Pred. No. 3.27e-61;
                           9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "novel antigenic peptides contain sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in diagnosis, vaccination and treatment
                           2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies and in vaccines against HCV. Sequence 191 AA;
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                   Jr 13
R44010 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                     capsid protein; vaccine; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= immunodominant_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 24pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.2%;
Best Local Similarity 89.9%;
Query Match 99.2%;
Best Local Similarity 89.9%;
                                                                                                                                                                                                                           12-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                              98; Conservative
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06-MAY-1992; FR-005763.
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                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                        /note= "peptide 1"
                                                                                                                                                                                                                                                                                                                                                                                 /note= "peptide 2"
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "peptide 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from this region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DALB/) DALBON P.
                                                                                                                                                                                                                                                                                                                                                                                                Peptide
/label= R40R
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                                                                                                                                                                                                                                                                                                                                                                     /label= P42Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalbon P,
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                                                                                                                                                         Hepatitis C virus isolate S14 core protein.
HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
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R92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genctyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to determine HCV genotype and as vaccines against HCV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                saliva, lymphocytes or other mononuclear cells. The antibodies may
                                                                                                                                                                                                                                                                                                                                                                                        DNA and amino acid sequence of HCV envelope 1 and core proteins
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Pred. No. 3.27e-61;
61 rrqpipkarrpegrtwaqpgypwplygnegcgwagwllsprgsrpswgp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRQPIPKAXRXEGRS#AQPGYPWPLYGNEGGGWAXWLLSPRGSRPNWGP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used in the prevention of HCV infection. Sequence 191 AA;
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                                                                                                     R92938 standard; Protein; 191 AA.
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Best Local Similarity 89.9%;
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                                                                                                                                       02-0CT-1996 (first entry)
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WPI; 96-139709/14.
N-PSDB; T16612.
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                                                                                                                                                                                                                                              22-FEB-1996.
15-AUG-1995; J10398.
                                                                                                                                                                                                             Hepatitis C virus. W09605315-A2.
                                                                                                                                                                                              hepatitis.
                                                                                                                        R92938;
                                                                                        RESULT
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pHCV141; amyloid precursor protein; APP; hepatitis C virus; HCV; El;

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R79222 standard; Protein; 967

(first entry)

08-DEC-1995

R79222;

pHCV141-encoded sequence.

E2; fusion protein; HEK-293; vaccine; vector; pRc/CMV;

protein secretion; glycosylation.

Synthetic. WO9520664-A.

ID DAYCE WERE TO DE TO D

03-AUG-1995.

Yamaguchi J;

Desai SM, Devare SG, Watanabe S,

27-JAN-1995; U01087. 28-JAN-1994; US-188281. (ABBO) ABBOTT LAB.

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T protein

S Disclosure; Page 59-62; 89pp; English.

Converted to Dlasma of a chimpanzee infected with HCV was converted to cDNA and PCR amplified using primers based on HCV converted to cDNA and PCR amplified using primers based on HCV converted to cDNA and PCR amplified using primers based on HCV converted to CDNA and PCR amplified using primers based on HCV converted to English and pHCV150 (see R1923). Fragments (from 2 clones, pHCV116 (see R1921). This was used to construct converted to English proteins that were glycosylated and secreted from HEX-293 transfectants.
                             New mammalian expression systems for HCV proteins - express fusion proteins comprising amyloid precursor protein and HCV El and/or E2
WPI; 95-275449/36.
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ö 2; Mismatches 9; Indels 0; Gaps Query Match 99.2%; Score 775; DB 13; Length 967; Best Local Similarity 89.9%; Pred. No. 3.27e-61; Matches 98; Conservative 2; Mismatches 9; Indels (

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Search completed: Mon Feb 23 11:00:48 1998 Job time: 61 secs. Š